

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 20, 2004, 11:05:12 ; Search time 47 Seconds

(without alignments)  
2698.352 Million cell updates/sec

Title: US-10-018-418-4

Perfect score: 4276

Sequence: 1 MSSAVASASFLALASASPQ.....SWEHAKLYEDVLKAKYQW 799

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
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8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
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10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
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13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
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18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4276	100.0	799	AA1980.DAT	Wheat starch synth
2	4276	100.0	799	AA1981.DAT	Wheat starch synth
3	4075	95.3	799	AA1982.DAT	Wheat starch synth
4	4059.5	89.9	798	AA1983.DAT	Wheat starch synth
5	3826.5	89.5	802	AA1984.DAT	Modified barley st
6	3821	89.4	813	AA1985.DAT	Barley cultivar Mo
7	3799.5	88.9	812	AA1986.DAT	Barley line 292 st
8	3799.5	88.9	812	AA1987.DAT	Barley line MK6827
9	3106	72.6	597	AA1988.DAT	Wheat starch synth

10	281.5	65.8	732	24	ABU06122	Starch synthase II
11	2742	64.1	727	24	ABU06556	Maize starch synth
12	2432	56.9	669	19	AAW70893	Maize starch solub
13	2432	56.9	669	19	AAW56486	Zea mays solub s
14	2319.5	54.2	804	19	AAW70892	Maize starch solub
15	2314.5	54.1	698	19	AAW56487	Zea mays solub s
16	2314.5	54.1	698	24	ABU06123	Starch synthase II
17	2198.5	51.4	682	24	ABU06771	Maize starch synth
18	2186	51.1	466	23	AAW51865	Rice starch synth
19	2163	50.6	801	23	ABU32438	Typa latifolia st
20	2161.5	50.5	792	23	ABU32160	Herbicideally activ
21	2063	48.2	690	23	ABU32433	Curcuma zedoaria s
22	2033	47.5	379	24	ABU06573	Maize SSIIa glucan
23	2031	47.5	379	24	ABU06572	Maize SSIIa glucan
24	1940	45.4	379	24	ABU06571	Maize SSIIa glucan
25	1929	45.1	379	24	ABU06574	Maize SSIIa glucan
26	1851	36.3	492	24	ABU06127	Starch synthase fu
27	1455.5	34.0	358	24	ABU06103	Maize starch synth
28	1360	31.8	361	24	ABU06104	Maize starch synth
29	1347	31.5	458	24	ABU06128	Starch synthase fu
30	1336.5	31.3	350	24	ABU06570	Maize SSIIa glucan
31	1330	31.1	348	24	ABU06569	Maize SSIIa glucan
32	1222.5	28.6	340	24	ABU06099	Starch synthase II
33	1201.5	28.1	649	19	AAW38218	Maize starch synth
34	1200	28.1	647	20	AAW09004	Wheat starch solub
35	1180	27.6	215	24	ABU06788	Maize SSIIb glucan
36	1180	27.6	215	24	ABU06789	Maize SSIIb glucan
37	1180	27.6	215	24	ABU06791	Maize SSIIb glucan
38	1178	27.5	215	24	ABU06790	Maize SSIIb glucan
39	1175.5	27.5	652	23	ABU93595	Herbicideally activ
40	1174.5	27.5	756	21	AAW50818	Wheat soluble star
41	1164	27.2	217	24	ABU06513	Maize SSI glycosyl
42	1151	26.9	217	24	ABU06510	Maize SSI glycosyl
43	1145	26.8	217	24	ABU06508	Maize SSI glycosyl
44	1145	26.8	217	24	ABU06509	Maize SSI glycosyl
45	1145	26.8	217	24	ABU06511	Maize SSI glycosyl

## ALIGNMENTS

XX	RESULT 1
XX	AA837567
XX	ID AA837567 standard; Protein; 799 AA.
XX	
XX	AA837567;
XX	
XX	01-MAR-2001 (first entry)
XX	
XX	Wheat starch synthase II SEQ ID NO: 4.
XX	
XX	Wheat; starch synthase; SSII; SSIII; starch content; starch synthesis;
XX	food product; adhesive.
XX	
XX	Triticum aestivum.
XX	
XX	MO200066745-A1.
XX	
XX	09-NOV-2000.
XX	
XX	28-APR-2000; 2000MO-AU00385.
XX	
XX	
XX	29-APR-1999; 99AU-0000052.
XX	
XX	(CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX	(GOOD-) GOODMAN FIELDER LTD.
XX	(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX	
XX	Morell M, Li Z, Rahman S, Appels R;
XX	
XX	WPI, 2000-647602/62.
XX	DR N-ESDB; AAC86411.
XX	

PT Nucleic acid molecules encoding wheat starch synthase (WST)-I and  
 WT-II, useful in modifying plant starch content and/or composition -  
 Claim 19; Page 158-161; 21pp; English.

The present invention relates to novel protein and coding sequences from  
 wheat. The proteins are wheat starch synthases, designated SStI and  
 SStII. These can be used in the modification of plant starch content or  
 composition, and to screen plants to identify mutations which affect  
 starch content and composition. The starch can then be used in food  
 products, such as flour, and in films, coatings, adhesives, building  
 materials and packaging materials.

Sequence 799 AA:

Query Match 100.0%; Score 4276; DB 21; Length 799;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSAVSAASFLALASAPGSRARRARVSAAPPHAGAGRLHMPMPORRTARDGGVAAARA 60  
 DB 1 MSSAVSAASFLALASAPGSRARRARVSAAPPHAGAGRLHMPMPORRTARDGGVAAARA 60  
 QY 61 AGKKDARVDDDAASAROPRARRGGAATKYAERDVPYKTLDRDAEAGAPAPAPRODAR 120  
 DB 61 AGKKDARVDDDAASAROPRARRGGAATKYAERDVPYKTLDRDAEAGAPAPAPRODAR 120  
 QY 121 PPSMNGTPVNGENKSTGGGATKDSGLPAPAPHPSTQNRVPVNGENKANYASPTSTIA 180  
 DB 121 PPSMNGTPVNGENKSTGGGATKDSGLPAPAPHPSTQNRVPVNGENKANYASPTSTIA 180  
 QY 181 EVVAPDSAAITISIDKAPESVVPAAKPPSSGSNFTVVSAPRLTDSVPEELKKGAVI 240  
 DB 181 EVVAPDSAAITISIDKAPESVVPAAKPPSSGSNFTVVSAPRLTDSVPEELKKGAVI 240  
 QY 241 VEEAPNPKALSPAPAAVOEDLMDPKKYIGFEEPEYAKDGMVAADAGSFEHQNHDSG 300  
 DB 241 VEEAPNPKALSPAPAAVOEDLMDPKKYIGFEEPEYAKDGMVAADAGSFEHQNHDSG 300  
 QY 301 PLAGENWNNVVVAACSPWCKTGGLDVAAGALPKALAKGHRVNVVPRGYEEAYDV 360  
 DB 301 PLAGENWNNVVVAACSPWCKTGGLDVAAGALPKALAKGHRVNVVPRGYEEAYDV 360  
 QY 361 GVRKTYKRAAGDMVNTYHATIDGVDFEIDAPLFRHROEDYVGSROETMKMILFCKA 420  
 DB 361 GVRKTYKRAAGDMVNTYHATIDGVDFEIDAPLFRHROEDYVGSROETMKMILFCKA 420  
 QY 421 AVEVPMHVPCCGVPYGDNLVFIANDWHTALLPYLKAYYRDHGLMQYTSIMVYINIAH 480  
 DB 421 AVEVPMHVPCCGVPYGDNLVFIANDWHTALLPYLKAYYRDHGLMQYTSIMVYINIAH 480  
 QY 481 OGRGVDSFPTELPENTLEHFRLYDPVGGHANYFAAGLMAOVVVSPGYMEKTV 540  
 DB 481 OGRGVDSFPTELPENTLEHFRLYDPVGGHANYFAAGLMAOVVVSPGYMEKTV 540  
 QY 541 EGGWGLHDIIRONDKTRGIWNGIDNMENPEVDVHLKSDGYTFSLGTLDGSRCKEA 600  
 DB 541 EGGWGLHDIIRONDKTRGIWNGIDNMENPEVDVHLKSDGYTFSLGTLDGSRCKEA 600  
 QY 601 LOREIGLOVRADVPLIGTIGRLDGOKYIETADAMPVVSODVQVLMGTRHDLSESLR 660  
 DB 601 LOREIGLOVRADVPLIGTIGRLDGOKYIETADAMPVVSODVQVLMGTRHDLSESLR 660  
 QY 661 HFEREHDKVRWGVFSVYLAHRTAGADALIMPSEPCGINSQLYAMAYGTVPVAVG 720  
 DB 661 HFEREHDKVRWGVFSVYLAHRTAGADALIMPSEPCGINSQLYAMAYGTVPVAVG 720  
 QY 721 GVRDTPPPDPNNHSGLGTFRPAAHKLTEALGSCLTATYDYESKNGLOERGSDQFS 780  
 DB 721 GVRDTPPPDPNNHSGLGTFRPAAHKLTEALGSCLTATYDYESKNGLOERGSDQFS 780  
 QY 781 WEHAATLYEDVLLKAKYQW 799

DB 781 WEHAATLYEDVLLKAKYQW 799

# RESULT 2

AAAB37597 standard; Protein; 799 AA.

AAAB37597;

01-MAR-2001 (first entry)

Wheat starch synthase II protein.

Wheat; starch synthase; SStI; SStII; starch content; starch synthesis;

food product; adhesive.

Triticum aestivum.

MO20006745-A1.

09-NOV-2000.

28-APR-2000; 2000WO-AU00365.

29-APR-1999; 99AU-0000052.

(CSTR) COMMONWEALTH SCI & IND RES ORG.

(GOOD-) GOODMAN FIELDER LTD.

(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.

Morell M, Li Z, Rahman S, Appels R;

WPI; 2000-647602/62.

Nucleic acid molecules encoding wheat starch synthase (WST)-I and  
 WST-II, useful in modifying plant starch content and/or composition -

Example 9; Fig 3; 21pp; English.

The present invention relates to novel protein and coding sequences from  
 wheat. The proteins are wheat starch synthases, designated SStI and  
 SStII. These can be used in the modification of plant starch content or  
 composition, and to screen plants to identify mutations which affect  
 starch content and composition. The starch can then be used in food  
 products, such as flour, and in films, coatings, adhesives, building  
 materials and packaging materials.

Sequence 799 AA:

Query Match 100.0%; Score 4276; DB 21; Length 799;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSAVSAASFLALASAPGSRARRARVSAAPPHAGAGRLHMPMPORRTARDGGVAAARA 60  
 DB 1 MSSAVSAASFLALASAPGSRARRARVSAAPPHAGAGRLHMPMPORRTARDGGVAAARA 60  
 QY 61 AGKKDARVDDDAASAROPRARRGGAATKYAERDVPYKTLDRDAEAGAPAPAPRODAR 120  
 DB 61 AGKKDARVDDDAASAROPRARRGGAATKYAERDVPYKTLDRDAEAGAPAPAPRODAR 120  
 QY 121 PPSMNGTPVNGENKSTGGGATKDSGLPAPAPHPSTQNRVPVNGENKANYASPTSTIA 180  
 DB 121 PPSMNGTPVNGENKSTGGGATKDSGLPAPAPHPSTQNRVPVNGENKANYASPTSTIA 180  
 QY 181 EVVAPDSAAITISIDKAPESVVPAAKPPSSGSNFTVVSAPRLTDSVPEELKKGAVI 240  
 DB 181 EVVAPDSAAITISIDKAPESVVPAAKPPSSGSNFTVVSAPRLTDSVPEELKKGAVI 240  
 QY 241 VEEAPNPKALSPAPAAVOEDLMDPKKYIGFEEPEYAKDGMVAADAGSFEHQNHDSG 300  
 DB 241 VEEAPNPKALSPAPAAVOEDLMDPKKYIGFEEPEYAKDGMVAADAGSFEHQNHDSG 300

QY 301 PLAGENNNVVVVAACSPCKTGGLGVAGALPKALAKRGHVVVVPRGYDEAYDV 360  
DB 301 PLAGENNNVVVVAACSPCKTGGLGVAGALPKALAKRGHVVVVPRGYDEAYDV 360  
QY 361 GYRKYYKAAAGQDMENYFHAVIDGVFVFIDAPLFRRHROEDYIGSGRQEIIMKRMILFCKA 420  
DB 361 GYRKYYKAAAGQDMENYFHAVIDGVFVFIDAPLFRRHROEDYIGSGRQEIIMKRMILFCKA 420  
QY 421 AVEVPMHVPCCGVPGYDGNLVFIANDMHTALLPVYLKAYYRDHGLMOYTRSIMVHNIAH 480  
DB 421 AVEVPMHVPCCGVPGYDGNLVFIANDMHTALLPVYLKAYYRDHGLMOYTRSIMVHNIAH 480  
QY 481 QGRGVPDEFPFTELEPHYLHFRILYDPVGGEHANYFAAGLKMAQVYVVSPGYLMELKTV 540  
DB 481 QGRGVPDEFPFTELEPHYLHFRILYDPVGGEHANYFAAGLKMAQVYVVSPGYLMELKTV 540  
QY 541 EGGWGLHDIIRQNDWKTRGIIVNGIDNMENPEVDVHLKSDGYTNFSLGTLDSGRQCKEA 600  
DB 541 EGGWGLHDIIRQNDWKTRGIIVNGIDNMENPEVDVHLKSDGYTNFSLGTLDSGRQCKEA 600  
QY 601 LQRELGLOVRADVPILGFIGRLDGQKVEIADAMPMTVSQDVQLVMTGSRHDLSEMLR 660  
DB 601 LQRELGLOVRADVPILGFIGRLDGQKVEIADAMPMTVSQDVQLVMTGSRHDLSEMLR 660  
QY 661 HFEREHNDKVRGWGFSVRLAHRITAGADALLMPSRFPCCGILQYAAAYGVTVVHAHV 720  
DB 661 HFEREHNDKVRGWGFSVRLAHRITAGADALLMPSRFPCCGILQYAAAYGVTVVHAHV 720  
QY 721 GYNDTVPPPPFPHNSGCTFEDBAEAKLIEALGHCLRTYRDYKESMRGLOEGMSQDS 780  
DB 721 GYNDTVPPPPFPHNSGCTFEDBAEAKLIEALGHCLRTYRDYKESMRGLOEGMSQDS 780  
QY 781 WEHAAKLIEDVLLKAKYQW 799  
DB 781 WEHAAKLIEDVLLKAKYQW 799

## RESULT 3

AAW23938

ID AAW23938 standard; Protein: 799 AA.

AC AAW23938;

DT 21-MAY-1998 (first entry)

DE wheat granule-bound starch synthase.

KM Starch synthase; wheat; transgenic plant.

OS Triticum aestivum L. cv. Florida.

PN WO9745545-A1.

PD 04-DEC-1997.

PF 28-MAY-1997; 97MO-E202793.

PR 11-SEP-1996; 96DE-1036917.

PR 29-MAY-1996; 96DE-1021588.

PA (AGRE ) HOECHST-SCHERING AGREVO GMBH.

PI Block M, Loertz H, Luetliche S, Froberg C, Kosmann J;

DR WPI; 1998-032652/03.

DR N-PSDB; AAV01528.

PT Nucleic acid encoding starch synthase enzymes from wheat - for

PT transgenic plants that produce modified forms of starch, useful e.g.

PT in foods, or for production of packaging materials and disposable

PS Claim 1; Page 54-58; 71pp; English.  
XX This amino acid sequence comprises a full-length sequence for a  
XX granule-bound starch synthase of summer wheat (cv. Florida). It  
CC was deduced from a cDNA clone (AAV01528) isolated from a 21-day  
CC caryopsis cDNA library. A solubled starch synthase (see AAW23937)  
CC has also been identified. Isolated nucleic acids encoding these  
CC enzymes can be inserted into vectors for production of transgenic  
CC plants, particularly starch-producing plants, specifically wheat.  
CC Use of the isolated nucleic acids, or of antisense sequences, allows  
CC starch metabolism to be regulated in transgenic plants.  
CC Overexpression may result in improved crop yield, while modification  
CC of starch in plants may eliminate the need for subsequent  
CC chemical/physical modification. Plants with altered levels of the  
CC various isoforms of starch synthase will produce starch of different  
CC chain length, amylose/amylopectin ratio, degree of branching,  
CC phosphate content, gelatinisation behaviour, granule size and shape,  
CC viscosity etc. The starch produced by such plants is useful  
CC particularly in foods (especially bakery goods and pasta) or to  
CC produce packaging materials or disposable goods, as well as in any  
CC other known use of starch.  
SQ Sequence 799 AA;

Query Match 95.3%; Score 4075; DB 19; Length 799;  
Best Local Similarity 95.6%; Pred. No. 0;  
Matches 764; Conservative 7; Mismatches 28; Indels 0; Gaps 0;

QY 1 MSSAVASASFLALASAPGSRRARAVSAPPFPAAGARLHMPWPQRTARDGVAAARA 60  
DB 1 MSSAVASASFLALASAPGSRRARAVSAPPFPAAGARLHMPWPQRTARDGVAAARA 60  
QY 61 AGKQDARVDDAASAROPRARAGGAATKVAERKDPVTLDRDAEGGAPAPARQDAAR 120  
DB 61 AGKQDAGIDDAASAROPRARAGGAATKVAERKDPVTLDRDAEGGAPAPARQDAAR 120  
QY 121 PPSNMGTPVNGENKSTGGGATKDSGLPAPARAPHPSTONKVPVNGENKANVASPPTISA 180  
DB 121 PPSNMGTPVNGENKSTGGGATKDSGLPAPARAPHPSTONKVPVNGENKANVASPPTISA 180  
QY 161 EVVAPDSAAATISIDKAESEVVPKOPPS3SNFVVASAPRLDIDSYVEPELKKGAVI 240  
DB 161 EVVAPDSAAATISIDKAESEVVPKOPPS3SNFVVASAPRLDIDSYVEPELKKGAVI 240  
QY 241 VEEAPNPKALSPPAPAPVQEDLMDPKYIG3EEVVEAKDDQWAAVADAGSEHHQNDISG 300  
DB 241 VEEAPNPKALSPPAPAPVQEDLMDPKYIG3EEVVEAKDDQWAAVADAGSEHHQNDISG 300  
QY 301 PLAGENNNVVVVAACSPCKTGGLGVAGALPKALAKRGHVVVVPRGYDEAYDV 360  
DB 301 PLAGENNNVVVVAACSPCKTGGLGVAGALPKALAKRGHVVVVPRGYDEAYDV 360  
QY 361 GYRKYYKAAAGQDMENYFHAVIDGVFVFIDAPLFRRHROEDYIGSGRQEIIMKRMILFCKA 420  
DB 361 GYRKYYKAAAGQDMENYFHAVIDGVFVFIDAPLFRRHROEDYIGSGRQEIIMKRMILFCKA 420  
QY 421 AVEVPMHVPCCGVPGYDGNLVFIANDMHTALLPVYLKAYYRDHGLMOYTRSIMVHNIAH 480  
DB 421 AVEVPMHVPCCGVPGYDGNLVFIANDMHTALLPVYLKAYYRDHGLMOYTRSIMVHNIAH 480  
QY 481 QGRGVPDEFPFTELEPHYLHFRILYDPVGGEHANYFAAGLKMAQVYVVSPGYLMELKTV 540  
DB 481 QGRGVPDEFPFTELEPHYLHFRILYDPVGGEHANYFAAGLKMAQVYVVSPGYLMELKTV 540  
QY 541 EGGWGLHDIIRQNDWKTRGIIVNGIDNMENPEVDVHLKSDGYTNFSLGTLDSGRQCKEA 600  
DB 541 EGGWGLHDIIRQNDWKTRGIIVNGIDNMENPEVDVHLKSDGYTNFSLGTLDSGRQCKEA 600  
QY 601 LQRELGLOVRADVPILGFIGRLDGQKVEIADAMPMTVSQDVQLVMTGSRHDLSEMLR 660  
DB 601 LQRELGLOVRADVPILGFIGRLDGQKVEIADAMPMTVSQDVQLVMTGSRHDLSEMLR 660  
QY 661 HFEREHNDKVRGWGFSVRLAHRITAGADALLMPSRFPCCGILQYAAAYGVTVVHAHV 720

Db 661 HFEREHDKVRGWFVRLAHRITAGADALMPSPFPCGLNQLYAMAYGVVPHAVG 720  
 Qy 721 GVRTPVPFPFPHNSGIGWTFDRAAHKLTALGHCTRTYRDYKESWGGLQERGMGSDPS 780  
 Db 721 GLRDTVPFPFPHNSGIGWTFDRAAHKLTALGHCTRTYRDYKESWGGLQERGMGSDPS 780  
 Qy 781 WEHAKLYEDVLLKAKYQW 799  
 Db 781 WEHAKLYEDVLLKAKYQW 799  
 RESULT 4  
 AAB37566  
 ID AAB37566 standard; Protein; 798 AA.  
 AC AAB37566;  
 XX  
 DT 01-MAR-2001 (first entry)  
 XX  
 DE Wheat starch synthase II SEQ ID NO: 2.  
 XX  
 XX Wheat; starch synthase; SSII; SSII; starch content; starch synthesis;  
 KW food product; adhesive.  
 XX  
 OS Triticum aestivum.  
 XX  
 FN WO20066745-A1.  
 XX  
 PD 09-NOV-2000.  
 XX  
 PF 28-APR-2000; 2000WO-AU00385.  
 XX  
 PR 29-APR-1999; 99AU-0000052.  
 XX  
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
 PA (GOOD-) GOODMAN FIELDER LTD.  
 PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.  
 XX  
 PI Morell M, Li Z, Rahman S, Appels R;  
 DR WPI: 2000-647602/62.  
 DR N-PSDB; AAC86410.  
 XX  
 PT Nucleic acid molecules encoding wheat starch synthase (WST)-I and  
 PT WST-II, useful in modifying plant starch content and/or composition -  
 PS Claim 19; Page 152-155; 211pp; English.  
 XX  
 CC The present invention relates to novel protein and coding sequences from  
 CC wheat. The proteins are wheat starch synthases, designated SSII and  
 CC SSIII. These can be used in the modification of plant starch content or  
 CC composition, and to screen plants to identify mutations which affect  
 CC starch content and composition. The starch can then be used in food  
 CC products, such as flour, and in films, coatings, adhesives, building  
 CC materials and packaging materials.  
 CC  
 SQ Sequence 798 AA;  
 Qy Query Match 94.9%; Score 4059.5; DB 21; Length 798;  
 Best Local Similarity 95.7%; Pred. No. 0;  
 Matches 765; Conservative 8; Mismatches 25; Indels 1; Gaps 1;  
 Db 1 MSSAVASASFLALASASGSRARRARVAPPHAGAGLHMPPPQRTARDGAVARA 60  
 1 MSSAVASASFLALASASGSRARRARVAPPHAGAGLHMPPPQRTARDGAVARA 60  
 Qy 61 AGKKDARVDDAASARQPARRGGAATKYAERRDPVKTLDRAAGAGAPAPAPRODAAR 120  
 61 AGKKDAGI-DDAAPARQPARALRGGAATKYAERRDPVKTLDRAAGAGAPAPAPRODAAR 119  
 Db 61 AGKKDAGI-DDAAPARQPARALRGGAATKYAERRDPVKTLDRAAGAGAPAPAPRODAAR 119  
 Qy 121 PRSMNGTVPNGENKSTGGGATKDSGLPAPAPAPRSTQKRVNNGENKANTASPTSTA 180  
 121 PRSMNGTVPNGENKSTGGGATKDSGLPAPAPAPRSTQKRVNNGENKANTASPTSTA 180

Db 120 LPSNMGMEVNGENKSTGGGATKDSGLPAPAPAPRSTQKRVNNGENKANTASPTSTA 179  
 Qy 181 EVAAPDSAAATISIDKAPESVVPAPKPPSSG3SNFVVSASAPRLDIDSVEPEIKKAVI 240  
 Db 180 EVAAPDPAAATISIDKAPESVVPAPKPPSSG3SNFVVSASAPSDTVSDVELEKKAVI 239  
 Qy 241 VEEANPAAATISIDKAPESVVPAPKPPSSG3SNFVVSASAPSDTVSDVELEKKAVI 300  
 Db 240 VEEANPAAATISIDKAPESVVPAPKPPSSG3SNFVVSASAPSDTVSDVELEKKAVI 299  
 Qy 301 PLAGENMNVVVVAAECSPMCKTGGLGDAVALPKALAKRGHRVNVVPRGYEAYDV 360  
 Db 300 PLAGENMNVVVVAAECSPMCKTGGLGDAVALPKALAKRGHRVNVVPRGYEAYDV 359  
 Qy 361 GVRKTYKAAAGDMEVNYTHAYIDGVDFVFIAPLFRHQEDIIYGSRQEIKKRMILPCKA 420  
 Db 360 GVRKTYKAAAGDMEVNYTHAYIDGVDFVFIAPLFRHQEDIIYGSRQEIKKRMILPCKA 419  
 Qy 421 AVEVPMHVPCCGVPYGDGNTLVFIANDMHTALLPVYLKAYRDHGLMQYTRSINVINHIAH 480  
 Db 420 AVEVPMHVPCCGVPYGDGNTLVFIANDMHTALLPVYLKAYRDHGLMQYTRSINVINHIAH 479  
 Qy 481 QGRGVDPEPFTLEPEHLEHFRLYDPVGEHANYFAAGLQADQVYVVSFGLMELKTV 540  
 Db 480 QGRGVDPEPFTLEPEHLEHFRLYDPVGEHANYFAAGLQADQVYVVSFGLMELKTV 539  
 Qy 541 EGGWGLHDIIRONDWTRGIVNGIDNMEMNEEVDVHLKSDGYTNSLGTLDGSKRCKEA 600  
 Db 540 EGGWGLHDIIRONDWTRGIVNGIDNMEMNEEVDVHLKSDGYTNSLGTLDGSKRCKEA 599  
 Qy 601 LQREIGLQVRADVPLIGTIGRIDGQKGYEIIADAMPVISOVQVLMGTGRHDESLR 660  
 Db 600 LQREIGLQVRADVPLIGTIGRIDGQKGYEIIADAMPVISOVQVLMGTGRHDESLR 659  
 Qy 661 HFEREHDKVRGWFVRLAHRITAGADALMPSPFPCGLNQLYAMAYGVVPHAVG 720  
 Db 660 HFEREHDKVRGWFVRLAHRITAGADALMPSPFPCGLNQLYAMAYGVVPHAVG 719  
 Qy 721 GVRDTVPFPFPHNSGIGWTFDRAAHKLTALGHCTRTYRDYKESWGGLQERGMGSDPS 780  
 Db 720 GLRDTVPFPFPHNSGIGWTFDRAAHKLTALGHCTRTYRDYKESWGGLQERGMGSDPS 779  
 Qy 781 WEHAKLYEDVLLKAKYQW 799  
 Db 780 WEHAKLYEDVLLKAKYQW 798  
 RESULT 5  
 AAU99845  
 ID AAU99845 standard; Protein; 802 AA.  
 AC AAU99845;  
 XX  
 DT 07-OCT-2002 (first entry)  
 XX  
 DE Modified barley starch synthase II (SSII).  
 XX  
 KW Barley; starch synthase II; SSII; high amylose; reduced amylopectin;  
 KW food production; swelling volume; gelatinisation temperature;  
 KW reduced swelling; reduced viscosity; low crystallinity; instant noodle;  
 KW v form starch crystallinity; dietary fibre; instant soup.  
 XX  
 OS Hordeum vulgare.  
 XX  
 FT Key Location/Qualifiers  
 FT Misc-difference 140 /note= "Encoded by GCC"  
 FT Misc-difference 716 /note= "Encoded by GTC"  
 FT  
 XX  
 FN WO200237955-A1.  
 XX  
 PD 16-MAY-2002.



XX 09-NOV-2001; 2001MO-AU01452.  
PF 09-NOV-2000; 2000AU-0001370.  
XX 09-NOV-2000; 2000AU-0001371.  
PR 09-NOV-2000; 2000AU-0001372.  
PR 09-NOV-2000; 2000AU-0001373.  
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
PA Morell MK, Topping D, Batey IL;  
PI WPI; 2002-557434/59.  
XX N-PSDB; ABR88112.  
DR N-PSDB; ABR88112.  
XX New barley plant for producing starch with improved characteristics,  
PT has reduced level of SSII activity and is capable of bearing grain -  
XX  
XX Example 1; Fig 12, 107pp; English.  
XX The invention describes a barley plant (I) with a reduced level of starch  
XX synthase II (SSII) activity and capable of bearing grain, where the  
XX starch of the grain has a high amylose content by reason of a reduced  
XX amylopectin content and the grain (I) is suitable for food production. (I),  
XX the starch (II) and the grain (III) are useful for food products, in  
XX food processing procedures, and in dietary and food processing  
XX applications. (II) has reduced amylopectin content, and relatively high  
XX amylose content. (I) exhibits a low swelling volume (2.0-3.2). The  
XX grain has relatively high beta-glucan content. (II) has low  
XX gelatinisation temperature, reduced swelling, reduced viscosity and low  
XX crystallinity. The starch also has high levels of lipid exhibiting very  
XX high levels of V form starch crystallinity. The dietary fibre content of  
XX the starch is high. The starch thus provides a prospect of significantly  
XX enhancing the nutritional benefits of foods, where there is a requirement  
XX of rapid preparation, such as instant soups and instant noodles. This  
XX is the amino acid sequence of the starch synthase II with reduced  
XX activity described in the invention.  
XX  
XX Sequence 802 AA;  
SQ Query Match 89.5%; Score 3826.5; DB 23; Length 802;  
Best Local Similarity 90.0%; Pred. No. 1.6e-302;  
Matches 730; Conservative 17; Mismatches 43; Indels 21; Gaps 4;  
QY 1 MSSAVASAFSLAASAPGR-SRRRARVSAPEPHAGAGLHNPMPPOSTADGGVAAR 59  
DB 1 MSSAVASAFSLAASAPGRSRRRARVSAPEPHAGAGLHNPMPPOSTADGGVAAR 60  
QY 60 AAGKKDARVDDDAASARQPRARSGAATKVAERDVKTLDRDAEGGAPAPAPRODA 119  
DB 61 AAG-----IDDAAPGQPRARFGAATKVA---DPVKTLDRDAEGGAPAPAPRODA 111  
QY 120 RPPPMNGPVPVNGENKSTGGGATGSGLPAPAPAPHSTQNVVNENKANYASPTST 179  
DB 112 RLPSTNGTLLINGENKPTGGGATGSGLPAPAPAPHSTQNVVNENKANYASPTST 171  
QY 180 AEVAPDAAATISIDKAPESVPAEKPP-----PSSGNTFVSAAPRLDIDS 228  
DB 172 VDVASPGSAANISINKNVPSPVPAKTPSSVPAKKTLPSSGNTFVSAAPRLDIDS 231  
QY 229 DVEPELKAGATVEBAEPKALSPAPAAVOEDLMDPKTYGFEPEPEADDDGAAVADA 268  
DB 232 DVEIAQKDALIVEAPKALSPAPAAVOEDLMDPEKTYGFEPEPEADDDGAAVADA 291  
QY 289 GSFEHQNHDGSLAGENVMVVAACSPWCKTGIGADVAGALPYALARGHRVWVV 348  
DB 292 GSFEHQNHDGSLAGENVMVVAACSPWCKTGIGADVAGALPYALARGHRVWVV 351  
QY 349 PRYGDYEAAVDGKATYKKAAGQDMVVFYHAYIDGVFVITADLPFRHREDDYGGSRQ 408  
DB 352 PRYGDYEAAVDGKATYKKAAGQDMVVFYHAYIDGVFVITADLPFRHREDDYGGSRQ 411  
QY 409 EIMKRMILFCKAAVEVMWHPCCGVYPGQGNLVPFIANDMHTALLPYLKAAYVNDHGLMOY 468  
DB 412 EIMKRMILFCKAAVEVMWHPCCGVYPGQGNLVPFIANDMHTALLPYLKAAYVNDHGLMOY 471  
QY 469 TRSTMTVHNIAHORGVDPEFPTELPEHYLEHFRLYDPVGGSHANYFAAGLKADQVAV 528  
DB 472 SRSVMVHNIAHORGVDPEFPTELPEHYLEHFRLYDPVGGSHANYFAAGLKADQVAV 531  
QY 529 VSPGYLWELKTVEGWGLHDIIIRONDWKTGIVNGIDNEMNEPVDVHLKSDGYTFSLG 568  
DB 532 VSPGYLWELKTVEGWGLHDIIIRONDWKTGIVNGIDNEMNEPVDVHLKSDGYTFSLG 591  
QY 589 TLDSGKQCKEALQRELGLOVGDVPLGFTGRDQKGVETIADAMPVLSQDVQLVWL 648  
DB 592 TLDSGKQCKEALQRELGLOVGDVPLGFTGRDQKGVETIADAMPVLSQDVQLVWL 651  
QY 649 GTGRHDESLMRHFEREHDKVRGWSVRLAHRITAGADALLMPSEFPCCGINQLYAM 708  
DB 652 GTGRHDESLMRHFEREHDKVRGWSVRLAHRITAGADALLMPSEFPCCGINQLYAM 711  
QY 709 AYGTVPVHANGVGRDTPPPDPFNHSGLQMTDPRAHKLITELGHCITRDYKESWR 768  
DB 712 AYGTVPVHANGVGRDTPPPDPFNHSGLQMTDPRAHKLITELGHCITRDYKESWR 771  
QY 769 GLQERGMSQDPSMEHAALYEDVLLKAKYQW 799  
DB 772 GLQERGMSQDPSMEHAALYEDVLLKAKYQW 802  
XX  
XX RESULT 6  
XX AAU99844  
XX ID AAU9844 standard; Protein; 813 AA.  
XX  
XX AAU99844;  
XX 07-OCT-2002 (first entry)  
XX  
XX DE Barley cultivar Morex starch synthase II (SSII).  
XX  
XX KM Barley; starch synthase II; SSII; high amylose; reduced amylopectin;  
XX food production; swelling volume; gelatinisation temperature;  
XX reduced swelling; reduced viscosity; low crystallinity; instant noodle;  
XX V form starch crystallinity; dietary fibre; instant soup; cultivar Morex.  
XX  
XX OS Hordeum vulgare.  
XX  
XX PN MO200237955-AA.  
XX  
XX PD 16-MAY-2002.  
XX  
XX PF 09-NOV-2001; 2001MO-AU01452.  
XX  
XX PR 09-NOV-2000; 2000AU-0001370.  
XX PR 09-NOV-2000; 2000AU-0001371.  
XX PR 09-NOV-2000; 2000AU-0001372.  
XX PR 09-NOV-2000; 2000AU-0001373.  
XX  
XX PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
XX  
XX PI Morell MK, Topping D, Batey IL;  
XX  
XX DR WPI; 2002-557434/59.  
XX DR N-PSDB; ABR88112.  
XX  
XX PT New barley plant for producing starch with improved characteristics,  
XX has reduced level of SSII activity and is capable of bearing grain -  
XX  
XX XX Example 1; Fig 12, 107pp; English.  
XX The invention describes a barley plant (I) with a reduced level of starch  
XX synthase II (SSII) activity and capable of bearing grain, where the  
XX starch of the grain has a high amylose content by reason of a reduced  
XX amylopectin content and the grain (I) is suitable for food production. (I),  
XX the starch (II) and the grain (III) are useful for food products, in

CC food processing procedures, and in dietary and food processing  
CC applications. (ii) has reduced amylopectin content, and relatively high  
CC amylose content. (i) exhibits a low swelling volume (2.0-3.2). The  
CC grain has relatively high beta-glucan content. (ii) has low  
CC gelatinisation temperature, reduced swelling, reduced viscosity and low  
CC crystallinity. The starch also has high levels of lipid exhibiting very  
CC high levels of V form starch crystallinity. The dietary fibre content of  
CC the starch is high. The starch thus provides a prospect of significantly  
CC enhancing the nutritional benefits of foods, where there is a requirement  
CC of rapid preparation, such as instant soups and instant noodles. This  
CC is the amino acid sequence of the starch synthase II from barley cultivar  
CC Morex.

XX Sequence 813 AA;

Query Match 89.4%; Score 3921; DB 23; Length 813;  
Best Local Similarity 88.8%; Pred. No. 4.5e-302;  
Matches 730; Conservative 17; Mismatches 43; Indels 32; Gaps 4;

QY 1 MSAAVSAASFLALASASGR-SRRARVAPPNAGRLWMPMPORTARDGVAR 59  
DB 1 MSAAVSAASFLALASASGR-SRRARVAPPNAGRLWMPMPORTARDGVAR 60  
QY 60 AAGKDAVDDAASAROPARRGGAATVAREDPVKTLDPAABGAPAPAPRODA 119  
DB 61 AAG-----IDDAAPGRQPARRYGAATKVA--DEVKTLDDPALEGSPAPRODA 111  
QY 120 RPSNMGTPNGENKGTGGGATKDSGLAPAPAPHPSTONRVNGENKAVASPTSI 179  
DB 112 RPSNMGTPNGENKGTGGGATKDSGLAPAPAPHPSTONRVNGENKAVASPTSI 171  
QY 180 AEVAPDSAAITISIDVAPESVVAEKP-----DSSGSNFV 217  
DB 172 VDVAPESSANISINNVPPSVPAKTPSSVFAKPAKPPSSVPAKKTLPSSGSNFVS 231  
QY 218 SASAPRLDIDVPELKKANVVEAPNPKALSPAPAPVODLMDFKYIGFEEPVAA 277  
DB 232 SASAPRLDIDVPELKKANVVEAPNPKALSPAPAPVODLMDFKYIGFEEPVAA 291  
QY 278 KDDGMAVADDAGSEFHQNDGSLAGENVMNVVVAECSFWCKTGGIGDVAGALPKAL 337  
DB 292 KDDGMAVADDAGSEFHQNDGSLAGENVMNVVVAECSFWCKTGGIGDVAGALPKAL 351  
QY 338 AKRGHVVVVPRRGDYEAIVDVRKTYKAAQGDMEVNFHAYIGVDPVFIDAPLPH 397  
DB 352 AKRGHVVVVPRRGDYEAIVDVRKTYKAAQGDMEVNFHAYIGVDPVFIDAPLPH 411  
QY 398 ROEDYIGGSRQEIKKRMILFCKAIVEPMWPCGCVYGDONTVFANDWHTALLPYLK 457  
DB 412 ROEDYIGGSRQEIKKRMILFCKAIVEPMWPCGCVYGDONTVFANDWHTALLPYLK 471  
QY 458 AYRHDHGMQYTRSLMTVHTNAGQGRPVDFPTEPHYHFRYXDVGEHANYFA 517  
DB 472 AYRHDHGMQYTRSLMTVHTNAGQGRPVDFPTEPHYHFRYXDVGEHANYFA 531  
QY 518 AGLKADQVVVVSPCYLMEKLTVEGGMGLHDIIRQNDMKTGIVNGIDNNEWNEVDVHL 577  
DB 532 AGLKADQVVVVSPCYLMEKLTVEGGMGLHDIIRQNDMKTGIVNGIDNNEWNEVDVHL 591  
QY 578 KSDGYTNFSLGTLDGSKQCKEALORELGLQVRADVPLLGSTGLDQCKGVETIADMPW 637  
DB 592 KSDGYTNFSLGTLDGSKQCKEALORELGLQVRADVPLLGSTGLDQCKGVETIADMPW 651  
QY 638 IYSDQVQVLMGTGSHDLESMILRHERBHDKVGWVVFVRLAHRITAGADALLMPSRF 697  
DB 652 IYSDQVQVLMGTGSHDLESMILRHERBHDKVGWVVFVRLAHRITAGADALLMPSRF 711  
QY 698 EPCGJNOIYANAYGVTPVHVAVGVDTVPPEPDNNSGLGWTBPAHAHLIALGHCL 757  
DB 712 EPCGJNOIYANAYGVTPVHVAVGVDTVPPEPDNNSGLGWTBPAHAHLIALGHCL 771  
QY 758 RTYRDYKESWRGLQERGMQDPSWEHAALCYEDVLLKAYCW 799

DB 772 RTYRDYKESWRGLQERGMQDPSWEHAALCYEDVLLKAYCW 813

RESULT 7

AAU99846  
AAU99846 standard; Protein; 812 AA.

AAU99846;  
07-OCT-2002 (first entry)

Barley line 292 starch synthase II (SSI1).

Barley; starch synthase II; SSI1; high amylose; reduced amylopectin;  
food production; swelling volume; gelatinisation temperature;  
reduced swelling; reduced viscosity; low crystallinity; instant noodle;  
V form starch crystallinity; dietary fibre; instant soup; line 292.

Hordeum vulgare.

Key Location/Qualifiers  
Misc-difference 583  
/note= "Encoded by TGA"

W0200237955-A1.

16-MAY-2002.

09-NOV-2001; 2001WO-AUD1452.

09-NOV-2000; 2000AU-0001370.

09-NOV-2000; 2000AU-0001371.

09-NOV-2000; 2000AU-0001372.

09-NOV-2000; 2000AU-0001373.

(CSIR) COMMONWEALTH SCI & IND RES ORG.

Morell MK, Topping D, Batey IL;

WPI, 2002-557434/59.

N-PSDB; ABR86115.

New barley plant for producing starch with improved characteristics,  
has reduced level of SSI1 activity and is capable of bearing grain

Example 1; Fig 12; 107pp; English.

The invention describes a barley plant (i) with a reduced level of starch  
synthase II (SSI1) activity and capable of bearing grain, where the  
starch of the grain has a high amylose content by reason of a reduced  
amylopectin content and the grain is suitable for food production. (i),  
the starch (ii) and the grain (iii) are useful for food products, in  
food processing procedures, and in dietary and food processing  
applications. (ii) has reduced amylopectin content, and relatively high  
amylose content. (i) exhibits a low swelling volume (2.0-3.2). The  
grain has relatively high beta-glucan content. (ii) has low  
gelatinisation temperature, reduced swelling, reduced viscosity and low  
crystallinity. The starch also has high levels of lipid exhibiting very  
high levels of V form starch crystallinity. The dietary fibre content of  
the starch is high. The starch thus provides a prospect of significantly  
enhancing the nutritional benefits of foods, where there is a requirement  
of rapid preparation, such as instant soups and instant noodles. This  
is the amino acid sequence of the starch synthase II from barley line  
292.

Sequence 812 AA;

Query Match 88.9%; Score 3799.5; DB 23; Length 812;  
Best Local Similarity 88.7%; Pred. No. 2.5e-300;  
Matches 725; Conservative 17; Mismatches 43; Indels 33; Gaps 5;

QY 1 MSAAVSAASFLALASASGR-SRRARVAPPNAGRLWMPMPORTARDGVAR 59

Db 1 MSSAVASPAFLALASAPGSSRRRARVGSPTTAGAGLQWRPSPLORTARDGVAAR 60  
 Qy 60 AAGKDKARVDDDAASAROPARRGGAATKVAERBDVKTLDRAAAGGAPAPAPRODA 119  
 Xx 61 AAG-----IDDAAGRPARRRYGAATKVA---DVKTLDRDAAGGGSPAPRODA 111  
 Db 120 RPPSMNGTPVNGENKSTGGGATKDSGLPAPAPAPSTONRVPVNGENKANYASPPTSI 179  
 Qy 112 RLPSKNGTLINGENKPTGGGATKDSGLPAPAPAPSTONRVPVNGENKANYASPPTSI 171  
 Db 180 AEVYAPDSATTSISDAPESVYPAKRP-----PSSGNSPVY 217  
 Qy 172 VDVASPSSAANISISNKPVPSPVPAKTPPSSVFPAPKAPSSVPAKKTLPSSGNSPV 231  
 Db 218 SASAPRLDIDSDVEPELKKGAVIYEAPNPKALSPAPAOEDLMDPKYIGFEEPEVA 277  
 Qy 232 SASAPRLDITVSDVELAQKDALIYKAPKPKALSAPAPAVQEDLMDPKYIGFEEPEVA 291  
 Db 278 KDDGMAVADDAAGSFHHQNDSGPLAGENMANYVVAACSPCKTGGLGDAVAGALPKAL 337  
 Qy 292 KDDGSAVADDAAGSFHHQNDSGPLAGENMANYVVAACSPCKTGGLGDAVAGALPKAL 351  
 Db 338 AKGHRMNVVPPRGDYEEAYDVGRKYKAGQDMENVYFHAVIDGVDFVFDALFPH 397  
 Qy 352 AKGHRMNVVPPRGDYEEAYDVGRKYKAGQDMENVYFHAVIDGVDFVFDALFPH 411  
 Db 398 RQEDYIGSGROEIMKRMILFCKAAVEVPMHVPCCGVPGDNLVFIANDMHTALLPVYK 457  
 Qy 412 RQODYIGSGROEIMKRMILFCKAAVEVPMHVPCCGVPGDNLVFIANDMHTALLPVYK 471  
 Db 458 AYVRDHLMQYTRSIMVTHINIAHQGRGPVDEFPTELPETHLHPRLYDVGGEHANYFA 517  
 Qy 472 AYVRDHLMQYTRSIMVTHINIAHQGRGPVDEFPTELPETHLHPRLYDVGGEHANYFA 531  
 Db 518 AGLMADQVVVVSFGYLMELKTYEGGGLDIIKQNDMKTGIVNGIDMKNNEPVDVHL 577  
 Qy 532 AGLMADQVVVVSFGYLMELKTYEGGGLDIIKQNDMKTGIVNGIDMKNNEPVDVHL 590  
 Db 578 KSDGYTMSLGTLDGSGRCKEALQRELQVADVLLGFTIRLQCKGVETIADAMP 637  
 Qy 591 KSDGYTMSLGTLDGSGRCKEALQRELQVADVLLGFTIRLQCKGVETIADAMP 650  
 Db 638 IVSODVOLVMLGTRHDLLESMLRFFEREHDDKVRGWFVSRLAHRITAGADALLMPSR 697  
 Qy 651 IVSODVOLVMLGTRHDLLESMLRFFEREHDDKVRGWFVSRLAHRITAGADALLMPSR 710  
 Db 698 EPCGLNOLYMAVGTIVVHAAGVGRDTVPDPFPNNSGIGWTFDRAEAKLIEALGHL 757  
 Qy 711 EPCGLNOLYMAVGTIVVHAAGVGRDTVPDPFPNNSGIGWTFDRAEAKLIEALGHL 770  
 Db 758 RTYRDYKESWRLQERGMQDSFSEHAAKLYEDVTLAKTYQW 799  
 Qy 771 RTYRDYKESWRLQERGMQDSFSEHAAKLYEDVTLAKTYQW 812

RESULT 8  
 AAU9847 ID AAU9847 standard; Protein; 812 AA.  
 AAU9847; ID AAU9847; (first entry)  
 07-OCT-2002 (first entry)  
 Barley line MK6827 starch synthase II (SSIi).  
 Barley; starch synthase II; SSIi; high amylose; reduced amylopectin;  
 food production; swelling volume; gelatinisation temperature;  
 reduced swelling; reduced viscosity; low crystallinity; instant noodle;  
 V form starch crystallinity; dietary fibre; instant soup.  
 Hordeum vulgare.  
 Location/Qualifiers  
 FH Key

FT Misc-difference 43 /note= "Encoded by TGA"  
 FT FT  
 FN MO20027955-A1.  
 Xx 16-MAY-2002.  
 PD 09-NOV-2001; 2001MO-AU01452.  
 PF 09-NOV-2000; 2000AU-0001370.  
 XX 09-NOV-2000; 2000AU-0001371.  
 PR 09-NOV-2000; 2000AU-0001372.  
 PR 09-NOV-2000; 2000AU-0001373.  
 XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 PA Morell MK, Topping D, Batey IL;  
 PI MPI-2002-557434/59.  
 XX N-PSDB; ABR86113.  
 DR New barley plant for producing starch with improved characteristics,  
 PT has reduced level of SSIi activity and is capable of bearing grain -  
 XX Example 1; Fig 12; 107pp; English.  
 PS The invention describes a barley plant (I) with a reduced level of starch  
 CC synthase II (SSIi) activity and capable of bearing grain, where the  
 CC starch of the grain has a high amylose content by reason of a reduced  
 CC amylopectin content and the grain is suitable for food production. (I),  
 CC the starch (II) and the grain (III) are useful for food products, in  
 CC food processing procedures, and in dietary and food processing  
 CC applications. (II) has reduced amylopectin content, and relatively high  
 CC amylose content. (I) exhibits a low swelling volume (2.0-3.2). The  
 CC grain has relatively high beta-glucan content. (II) has low  
 CC gelatinisation temperature, reduced swelling, reduced viscosity and low  
 CC crystallinity. The starch also has high levels of lipid exhibiting very  
 CC high levels of V form starch crystallinity. The dietary fibre content of  
 CC the starch is high. The starch thus provides a prospect of significantly  
 CC enhancing the nutritional benefits of foods, where there is a requirement  
 CC of rapid preparation, such as instant soups and instant noodles. This  
 CC is the amino acid sequence of the starch synthase II from barley line  
 CC MK6827.  
 CC XX  
 SQ Sequence 812 AA;  
 Query Match 88.9%; Score 3799.5; DB 23; Length 812;  
 Best Local Similarity 88.6%; Pred. No. 2.5e-300;  
 Matches 728; Conservative 18; Mismatches 43; Indels 33; Gaps 5;

Qy 1 MSSAVASPAFLALASAPGSSRRRARVGSPTTAGAGLQWRPSPLORTARDGVAAR 59  
 Db 1 MSSAVASPAFLALASAPGSSRRRARVGSPTTAGAGLQWRPSPLORTARDGVAAR 59  
 Qy 60 AAGKDKARVDDDAASAROPARRGGAATKVAERBDVKTLDRAAAGGAPAPAPRODA 119  
 Db 60 AAG-----IDDAAGRPARRRYGAATKVA---DVKTLDRDAAGGGSPAPRODA 110  
 Qy 120 RPPSMNGTPVNGENKSTGGGATKDSGLPAPAPAPSTONRVPVNGENKANYASPPTSI 179  
 Db 111 RLPSKNGTLINGENKPTGGGATKDSGLPAPAPAPSTONRVPVNGENKANYASPPTSI 170  
 Qy 180 AEVYAPDSATTSISDAPESVYPAKRP-----PSSGNSPVY 217  
 Db 171 VDVASPSSAANISISNKPVPSPVPAKTPPSSVFPAPKAPSSVPAKKTLPSSGNSPV 230  
 Qy 218 SASAPRLDIDSDVEPELKKGAVIYEAPNPKALSPAPAOEDLMDPKYIGFEEPEVA 277  
 Db 231 SASAPRLDITVSDVELAQKDALIYKAPKPKALSAPAPAVQEDLMDPKYIGFEEPEVA 290  
 Qy 278 KDDGMAVADDAAGSFHHQNDSGPLAGENMANYVVAACSPCKTGGLGDAVAGALPKAL 337  
 Db 291 KDDGSAVADDAAGSFHHQNDSGPLAGENMANYVVAACSPCKTGGLGDAVAGALPKAL 350

QY AKGHRVWVVPYGPVEEAYDVGVKRYKKAAGDMENVYEHAYIDGVFVFIADPLPRH 397  
 DB AKGHRVWVVPYGPVEEAYDVGVKRYKKAAGDMENVYEHAYIDGVFVFIADPLPRH 410  
 QY 398 ROEDIVGSSROEIMKRMILFCKAAVEVPMVPCGGVPGYDGNLVFIANDMHTALLPVYLK 457  
 DB 411 RQODIVGSSROEIMKRMILFCKAAVEVPMVPCGGVPGYDGNLVFIANDMHTALLPVYLK 470  
 QY 458 AAYPDHLMQYTRSIMTININAHQGRGVDPDEPPTLPEHYLHFLYDPVGGEHANYA 517  
 DB 471 AAYPDHLMQYTRSIMTININAHQGRGVDPDEPPTLPEHYLHFLYDPVGGEHANYA 530  
 QY 518 AGLKADQVWVVPYGPVMEKTVEGGGLHDIIRQNDMKTGIVNGIDNMENPEVDVHL 577  
 DB 531 AGLKADQVWVVPYGPVMEKTVEGGGLHDIIRQNDMKTGIVNGIDNMENPEVDVHL 590  
 QY 578 KSDGYTFSLGTLDGSKRQCKEALQRELGIQVADVPILGFIGRLDGQKVEIITADAMP 637  
 DB 591 KSDGYTFSLGTLDGSKRQCKEALQRELGIQVADVPILGFIGRLDGQKVEIITADAMP 650  
 QY 638 IVSDQVQVLMGTGRHDLSEMLRPFEREHHDKYRGWTFSVRLAHRITAGADALLMPSRF 697  
 DB 651 IVSDQVQVLMGTGRHDLSEMLRPFEREHHDKYRGWTFSVRLAHRITAGADALLMPSRF 710  
 QY 698 EPCGLNQLYMAVGTVPVVAHVGAVDTVPFPDPFNHSGIGWTFDRAEAKLIEALGHCL 757  
 DB 711 EPCGLNQLYMAVGTVPVVAHVGAVDTVPFPDPFNHSGIGWTFDRAEAKLIEALGHCL 770  
 QY 758 RTYRDYKESWRGLQERGMQDFSEWHAAKLYEDVILKAKYQW 799  
 DB 771 RTYRDYKESWRGLQERGMQDFSEWHAAKLYEDVILKAKYQW 812

RESULT 9  
 AAB37568  
 ID AAB37568 standard; Protein; 597 AA.

AC AAB37568;

DT 01-MAR-2001 (first entry)

DE Wheat starch synthase II SEQ ID NO: 6.

KW Wheat; starch synthase; SSII; SSII; starch content; starch synthesis;

KM food product; adhesive.

OS Triticum aestivum.

PN WO20006745-A1.

PD 09-NOV-2000.

PF 28-APR-2000; 2000MO-AU00385.

PR 29-APR-1999; 99AU-0000052.

PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

PA (GOOD-) GOODMAN FIELDER LTD.

PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.

PI Morell M, Li Z, Rahman S, Appels R;

DR WPI; 2000-647602/62.

DR N-PSDB; AAC66412.

PT Nucleic acid molecules encoding wheat starch synthase (WST)-I and

CC wheat. The present invention relates to novel protein and coding sequences from

CC SSII. These can be used in the modification of plant starch content or  
 CC composition, and to screen plants to identify mutations which affect  
 CC starch content and composition. The starch can then be used in food  
 CC products, such as flour, and in films, coatings, adhesives, building  
 CC materials and packaging materials.

SQ Sequence 597 AA:

Query Match 72.6%; Score 3106; DB 21; Length 597;

Best Local Similarity 96.3%; Pred. No. 4.9e-244;

Matches 575; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 203 PAEKPPSSGNSFPVVASAPRLDIDSDVEPELKKGAIVIEAPPKALSPPAAYVEDL 262  
 DB 1 PAEKPPSSGNSFPVVASAPRLDIDSDVEPELKKGAIVIEAPPKALSPPAAYVEDL 60  
 QY 263 WDFKKYIGFEEPPVEAKDGMVADAGSFEHQNHDSGPLAGENVWVVAACSPWCK 322  
 DB 61 WDFKKYIGFEEPPVEAKDGMVADAGSFEHQNHDSGPLAGENVWVVAACSPWCK 120  
 QY 323 TGGLDVAGALPKALKRGHVVVVPRYGYTEAIVYGRKYYKKAAGDMENVYEHAYI 382  
 DB 121 TGGLDVAGALPKALKRGHVVVVPRYGYTEAIVYGRKYYKKAAGDMENVYEHAYI 180  
 QY 383 DGVDVFETDAPLFRHROEDIVGSSROEIMKRMILFCKAAVEVPMVPCGGVPGYDGNLVF 442  
 DB 181 DGVDVFETDAPLFRHROEDIVGSSROEIMKRMILFCKAAVEVPMVPCGGVPGYDGNLVF 240  
 QY 443 IANDMHTALLPVYLKAYTRDHGLMQYTRSINVININAHQGRGVDPDEPPTLPEHYLHFL 502  
 DB 241 IANDMHTALLPVYLKAYTRDHGLMQYTRSINVININAHQGRGVDPDEPPTLPEHYLHFL 300  
 QY 503 RLYDPVGGEHANYFAAGKMAADQVWVVPYGPVMEKTVEGGGLHDIIRQNDMKTGIVN 562  
 DB 301 RLYDPVGGEHANYFAAGKMAADQVWVVPYGPVMEKTVEGGGLHDIIRQNDMKTGIVN 360  
 QY 563 GIDNMENPEVDVHLKSDGYTFSLGTLDGSKRQCKEALQRELGIQVADVPILGFIGRL 622  
 DB 361 GIDNMENPEVDVHLKSDGYTFSLGTLDGSKRQCKEALQRELGIQVADVPILGFIGRL 420  
 QY 623 DGQKVEIITADAMPWIVSQDVQVLMGTGRHDLSEMLRPFEREHHDKYRGWTFSVRLAH 682  
 DB 421 DGQKVEIITADAMPWIVSQDVQVLMGTGRHDLSEMLRPFEREHHDKYRGWTFSVRLAH 480  
 QY 683 RITAGADALLMPSRFPCGLNQLYMAVGTVPVVAHVGAVDTVPFPDPFNHSGIGWTFD 742  
 DB 481 RITAGADALLMPSRFPCGLNQLYMAVGTVPVVAHVGAVDTVPFPDPFNHSGIGWTFD 540  
 QY 743 RAFAKLTIEALGHCLRTYRDYKESWRGLQERGMQDFSEWHAAKLYEDVILKAKYQW 799  
 DB 541 RAFAKLTIEALGHCLRTYRDYKESWRGLQERGMQDFSEWHAAKLYEDVILKAKYQW 597

RESULT 10

ID ABOU06122 standard; Protein; 732 AA.

AC ABOU06122;

DT 17-FEB-2003 (first entry)

DE Starch synthase IId (SSIIb) glucan association domain (GLASS) #2.

KW Starch; starch synthase; glucan association domain; GLASS;

KM linker domain; LINKR; glucosyl transferase domain; GLYTR;

KM C-terminal end; CTEND; granule bound starch synthase; GBS;

OS morphology; retrogradation; waterbinding; swelling potential.

PN WO200279410-A2.

PD 10-OCT-2002.

XX 29-MAR-2002; 2002MO-US09574.  
 PF 30-MAR-2001; 2001US-279720P.  
 XX (BADI ) BASF PLANT SCI GMBH.  
 PA Commuri P, Keeling PL, Ramirez N, McKean A, Gao Z, Guan H;  
 XX WPI; 2003-040678/03.  
 DR  
 XX New DNA encoding fusion protein consisting of 4 different functional  
 PT domains selected from glucan association domain, linker domain,  
 PT glucosyl transferase domain, and C-terminal end, useful for producing  
 PT modified starches -  
 XX  
 PS Example 3; Page 125-126; 265pp; English.  
 CC The invention describes an isolated DNA molecule encoding a fusion  
 CC protein consisting of 4 different functional domains selected from  
 CC glucan association domain (GLASS), linker domain (LINKR), glucosyl  
 CC transferase domain (GLYTR), and C-terminal end (CTEND) which are  
 CC operably linked to one another. The DNA molecule is useful for  
 CC expressing in plants polypeptides including starch synthase enzymes as  
 CC fusion proteins with improved affinity to starch and modified catalytic  
 CC capabilities and to the in vivo and in vitro synthesis of glucan chains  
 CC of modified lengths as compared to plants producing native starch or  
 CC starch produced with native starch synthases. Expression of the starch  
 CC synthase fusion proteins along with granule bound starch synthase (GBSS)  
 CC will lead to a modified starch having an altered or improved morphology,  
 CC retrogradation, waterbinding, or swelling potential of the granules, gel  
 CC strength, adhesiveness, cohesiveness, hardness, elasticity, increased or  
 CC decreased granule size, degree of branching, crystallinity, degree of  
 CC cross-linking, and increased or decreased glucan chain lengths. This  
 CC is the amino acid sequence of a functional domain isolated from a  
 CC starch synthase.  
 CC  
 XX Sequence 732 AA;  
 SQ  
 Query Match 65.8%; Score 2811.5; DB 24; Length 732;  
 Best Local Similarity 68.2%; Pred. No. 6.3e-220;  
 Matches 550; Conservative 56; Mismatches 116; Indels 83; Gaps 10;  
 QY 1 MSSAVASAS---FLALASAPGRRARRAVSAPPFHAGR--LHWPMPORTARDG 55  
 DB 1 MSSAAVSSSSTFTLALASAPG-GRRRARVSSPFTGASLSPFAWAPSPPRARDAA 59  
 QY 56 V--AARAAGKDAVDVDDASAROPRARRGAAKVAERDPKXITLDRDAEGGAPRA 113  
 DB 60 LVRAEAEAGKDAPEPSSGDAARLPARRNA---VSKRDPLO----- 99  
 QY 114 PRODAAPPSPMNGTPVNGENKSTGGGATKDSGLPAPAKAPHSQNRVNGENKANYA 173  
 DB 100 -----PVRKYSATGN-----TARTGAASQQAALADVEIKSIYA 134  
 QY 174 SPPSISAEVVAAPSAAITISIDKAPESVVAPEKPPSSGSGNFVVSASAPLDDSDVEPE 233  
 DB 135 APPSISAEVVAAPSAAITISIDKAPESVVAPEKPPSSGSGNFVVSASAPLDDSDVEPE 233  
 QY 234 LKKAQAVIYEAPNPKALSPPA--PAVEDLMDFKKYTGFEPEVAKDGAADVADGASFE 292  
 DB 181 -----GIAPFVEPLVQEAETMDFKKYTGFEPEVAKDGSVADGADGASFE 225  
 QY 293 HHQNHDSGPTLAGEVNVVNVVAACSPWCKTGIGDVAGALPKALARGRRVNVVPRYG 352  
 DB 226 HYGNDHDSGPTLAGEVNVVNVVAACSPWCKTGIGDVAGALPKALARGRRVNVVPRYG 285  
 QY 353 DYEEAVDVGVRKYKKAAGQDMVVVPHAYIDGVFVFLDAPLPHRQEDYIGSGRQIYM 412  
 DB 286 DYVAFEDVGIRKYKKAAGQDMVVVPHAYIDGVFVFLDAPLPHRQEDYIGSGRQIYM 345  
 QY 413 RMILFCKAAVEVPMHVPQGVYDQGNLVFLANDMHTALLPVYIKAYYRDHGLMQYTRST 472

DB 346 RMILFCKAAVEVPMHVPQGVYDQGNLVFLANDMHTALLPVYIKAYYRDHGLMQYTRSV 405  
 QY 473 MVININIAHQSGPVDPEPFTELPEHYLEHPELXPVPGSEHANYPAALAKMADQVWVSPG 532  
 DB 406 LVININIAHQSGPVDPEPFTELPEHYLOHPELVYPVPGSEHANYPAALAKMADQVWVSPG 465  
 QY 533 YLMEIKTVGGWGLHDIIRQNDWKTGRIVNGIDNMENPEVDVHLKSDGTITNSLGLTDS 592  
 DB 466 YLMEIKTVGGWGLHDIIRQNDWKTGRIVNGIDNMENPEVDVHLKSDGTITNSLGLTDS 525  
 QY 593 GKQCKEALORELGLQVADVPILGFTGRDQJQGVETIDAMWIVSODVQLVMLGTGR 652  
 DB 526 GKQCKEALORELGLQVADVPILGFTGRDQJQGVETIDAMWIVSODVQLVMLGTGR 585  
 QY 653 HDLESMLHFEREHDKYRGVNGSVRLAHRITAGADALLMPSRPECGINQLYAMAAYGT 712  
 DB 586 ADLERMLOHLRERHPNKRGMVNGSVPMARHTAGADVLVMPSRPECGINQLYAMAAYGT 645  
 QY 713 VPVYHAGVGRDTPPDPENHSGLGWTFDRYEAHKLIEALGHCLRTYRDYKESGRGLOE 772  
 DB 646 VPVYHAGVGRDTPPDPENHSGLGWTFDRYEAHKLIEALGHCLRTYRDYKESGRGLOE 705  
 QY 773 RGMGQDFSMERAKLYEDVLKAKYQW 799  
 DB 706 RGMGQDFSMERAKLYEDVLKAKYQW 732  
 RESULT 11  
 AB06556  
 ID AB06556 standard; Protein; 727 AA.  
 XX  
 AC AB06556;  
 XX  
 DT 17-FEB-2003 (first entry)  
 XX  
 DE Maize Starch synthase IIa (SSIIa).  
 XX  
 KM Starch; starch synthase; glucan association domain; GLASS;  
 KM linker domain; LINKR; glucosyl transferase domain; GLYTR;  
 KM C-terminal end; CTEND; granule bound starch synthase; GBSS;  
 KM morphology; retrogradation; waterbinding; swelling potential.  
 XX  
 OS Zea mays.  
 XX  
 PN WO200279410-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 29-MAR-2002; 2002MO-US09574.  
 XX  
 PR 30-MAR-2001; 2001US-279720P.  
 XX  
 PA (BADI ) BASF PLANT SCI GMBH.  
 XX  
 PI Commuri P, Keeling PL, Ramirez N, McKean A, Gao Z, Guan H;  
 XX WPI; 2003-040678/03.  
 XX  
 DR  
 XX New DNA encoding fusion protein consisting of 4 different functional  
 PT domains selected from glucan association domain, linker domain,  
 PT glucosyl transferase domain, and C-terminal end, useful for producing  
 PT modified starches -  
 XX  
 PS Example 3; Page 158; 265pp; English.  
 CC The invention describes an isolated DNA molecule encoding a fusion  
 CC protein consisting of 4 different functional domains selected from  
 CC glucan association domain (GLASS), linker domain (LINKR), glucosyl  
 CC transferase domain (GLYTR), and C-terminal end (CTEND) which are  
 CC operably linked to one another. The DNA molecule is useful for  
 CC expressing in plants polypeptides including starch synthase enzymes as  
 CC fusion proteins with improved affinity to starch and modified catalytic  
 CC capabilities and to the in vivo and in vitro synthesis of glucan chains

CC of modified lengths as compared to plants producing native starch or  
CC starch produced with native starch synthases. Expression of the starch  
CC synthase fusion proteins along with granule bound starch synthase (GBSS  
CC will lead to a modified starch having an altered or improved morphology  
CC retrogradation, water-binding, or swelling potential of the granules, ge  
CC strength, adhesiveness, cohesiveness, hardness, elasticity, degree of  
CC decreased granule size, degree of branching, crystallinity, degree of  
CC cross-linking, and increased or decreased glucan chain lengths. This  
CC is the amino acid sequence of a starch synthase used in the creation of  
CC a starch synthase fusion protein

SQ Sequence 727 AA;

Query Match	64.1%;	Score	2742;	DB	24	Length	727;
Best Local Similarity	67.8%;	Pred. No.	2.9e-214				
Matches	577;	Conservative	57;	Mismatches	115;	Indels	88;
						Gaps	15;

[illegible]

RESULT 12

ID	AAW70893	standard; Protein; 669 AA.
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AC AAW70893;

DT 23-AUG-1999 (first entry)

DE Maize starch soluble synthase IIa

KM Non-glycogen-like polysaccharide production; fermentation;  
KM starch synthetase enzyme; glycogen synthetase  
KM non-starch branching gene; amylopectin; amylose; plant-like starch;  
KM maize starch soluble synthase IIa.

**Zea mays.**

PN WO9844780-A1.

PD 15-OCT-1998.

PF 03-APR-1998; 98WO-US066660.

PR 04-APR-1997; 97US-0042939.

PA (EXSE-) EXSEED GENETICS LLC.

PI Guan H, Keeling PL;

DR WPI; 1998-568285/48.

[illegible]

PT Producing non-glycogen-like polysaccharides in bacteria, fungi or plants - transformed with genes for enzymes involved in starch or glycogen synthesis allows fermentative production of starches with engineered properties

PS Disclosure; Fig 51; 150pp; English

The specification describes a method for the production of non-glycogen-like polysaccharides in a host. The method comprises transforming a host, suitable for fermentation, with genes encoding starch- or glycogen- synthesis enzymes, and fermenting the transformant. The specification also describes hosts transformed with a gene active in glycogen synthesis and at least one non-starch branching gene, involved in production of amylopectin or amylose in its original host. The method is used to produce plant-like starches by fermentation and new starches in plants. These starches are useful for all food and non-food applications of starch. The present sequence is used in the course of the invention.

**SQ** Sequence 669 AA;

Query Match	56.9%	Score 2432	DB 19	Length 669
Best Local Similarity	65.0%	Pred. No. 4.5e+189		
Matches 486	Conservative 58	Mismatches 120	Indels 84	Gaps 12

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QY      57 AARAAKCKDARVDDDAASAKROPARRGGATKTAHERDIPVYTLDRDAEAGSAPAPAPRQ 116
Db      1 AEMAEAGCKDAEPERSGDARLPARRNA-----VSGRDPELO----- 37
QY      117 DAAPPSMNGTPVNGENKSTGGGATKOSGLPAPAPAPSPSTONRVPN--GENKANVA 173
Db      38 -----PVGRRGSATGN-----TARGAACQNALADVAEIVAKSIVA 75
QY      174 SPTTSAIEVVAAPSAATITISDKAPESVVAPEKPPSSGSNFTVASAPFLDIDSVEFE 233
Db      76 APTSTIVKFPGRGLQDDPSLMDIAPETVLPAPKPLHES-----PAVDGDSN---- 121
QY      234 LKKAATVVEAPAPKALSPRAA-PAVQEDLMQFKKYITGFEEFVEKODGNAVADAGSFE 292
Db      122 -----GIAPTVVEPLVQEAETWQPFKKYIGFDEDEKANDSRGALDAGSFE 166

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QY 293 HHQNDSGPLAGENVNVAACSPWCKTGGLGVAGALPKALARGHRVNVVPRYG 352
D 167 HYGMWILG-LGGEVNVNVIIVAACSPWCKTGGLGVAGALPKALARGHRVNVVPRYG 225
QY 353 DYEAVGVGRKTYKAAAGQDMEVNYFHAVIDGVDFVIDA.PLRHROED.YGSSROEIMK 412
D 226 DYVAEAFWGIKRYKAAAGQDLEVVYFHAVIDGVDFVIDAS-FRRHRODDIYGSSROEIMK 284
QY 413 RMILFCKAAVEVPMHVPFCGVPYDGNLVFIANDMHTALLPVYLKAYYRDHGLMOYTRSI 472
D 285 RMILFCKAAVEVPMHVPFCGVPYDGNLVFIANDMHTALLPVYLKAYYRDHGLMOYTRSV 344
QY 473 MYIHNIAHOGRGVDEPFTELEPHYLEHFRLYDPVGGEHANTFAA-GLKMDQVYVVP 531
D 345 LVHINIGHOGRGVDEPFTELEPHYLEHFRLYDPVGGEHANTFAA-GLKMDQVYVVP 404
QY 532 GYLWEIKTVGSGMGLHDIIRONDWKTGIVNGIDNMENPEVDYHLKSDGTNFSIGTLD 591
D 405 GYLWEIKTVGSGMGLHDIIRONDWKTGIVNGIDNMENPEVDYHLKSDGTNFSIGTLD 464
QY 592 SGKROCKEALQRELGLQVADVPILGFTIGLDGQKVEIADAMPWISODVOLVMLGTG 651
D 465 AGKROCKAALQRELGLQVADVPILGFTIGLDGQKVEIADAMPWISODVOLVMLGTG 524
QY 652 RHDLESMTLHFRERHHDKVRGNGVGSVRLAHRTAGADALLMPSEFPDGLNLYAMA 711
D 525 PDLERMLQHLERHHPNKVRGNGVGSVRLAHRTAGADALLMPSEFPDGLNLYAMA 583
QY 712 TVPVHAAGVGRDTPPDPFENHSGLGWTFPDAENKLIIEALGHCLTRYDDYKESWGLQ 771
D 584 TVPVHAAGVGRDTPPDPFENHSGLGWTFPDAENKLIIEALGHCLTRYDDYKESWGLQ 643
QY 772 ERGMSQDSFWEHAALYEDVLLKAYQW 799
D 644 ARGMSQNSMDHAAELYEDVLL-KYQW 669

RESULT 13
ID AAM56486
AA AAM56486 standard; Protein; 669 AA.
AC AAM56486;
DT 11-SEP-1998 (first entry)
DE Zea mays soluble starch synthase IIa.
KM SER, starch-encapsulating region; fusion vector;
XX Soluble starch synthase IIa; glucosyl transferase.
OS Zea mays.
PN MO9814601-A1.
PD 09-APR-1998.
PF 30-SEP-1997; 97WO-US17555.
PR 30-SEP-1996; 96US-0026855.
PA (EXSE-) EXSEED GENETICS LLC.
PI Guan H, Keeling P;
XX WPI; 1998-240100/21.
DR N-PSDB; AAV29754.
PT Hybrid polypeptide comprising starch-encapsulating region and
PT protein--useful for, e.g. producing protein(s) resistant to
PS degradation by stomach acids
Example 2; Page 34-36; 156pp; English.

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XX CC The sequence is that of soluble starch synthase IIa.
CC CC it can be used in the production of a hybrid polypeptide
CC CC comprising a starch-encapsulating region (SER) fused
CC CC to a payload protein. The hybrid polypeptide can be used to make
CC CC modified starches comprising the payload protein, selected from,
CC CC e.g. hormones, growth factors, antibodies, enzymes, dyes,
CC CC immunoglobulins, etc. The modified starch can also be used
CC CC to provide grain feeds enriched in amino acids. By encapsulating
CC CC the payload protein in starch, it is more resistant to
CC CC degradation by stomach acids.
XX XX
SQ Sequence 669 AA;
Query Match 56.9%; Score 2432; DB 19; Length 669;
Best Local Similarity 65.0%; Pred. No. 4,5e-189;
Matches 486; Conservative 58; Mismatches 120; Indels 84; Gaps 12;
57 AABAAGKDAVDDDAASAPQRRARGGATKVAERDPVTLDRDAAGAPAPAPBRQ 116
D 1 AABAAGKDAVDDDAASAPQRRARGGATKVAERDPVTLDRDAAGAPAPAPBRQ 37
QY 117 DAARPPSNNGPVPNGENKSTGGGATKDSGLPAPAPAPHPTQNRVFN--GENKANVA 173
D 38 -----FVGRYGSATGN-----TARTGAACQVNAALDAIVEIKSIVA 75
QY 174 SPPTSLAEVNPDSATISISDKAPESVPAEKPPSSGSNFVSASAPRLDSDVEPE 233
D 76 APPTSLAEVNPDSATISISDKAPESVPAEKPPSSGSNFVSASAPRLDSDVEPE 121
QY 234 LKGAIVTEAENPRLSPAPAA-PAVQEDLWDFKXYIFEEPEVKAQDGMVADAGSFE 292
D 122 -----GIAPPTVEPLVQEAATWDFKXYIFEEPEVKAQDGMVADAGSFE 166
QY 293 HHQNDSGPLAGENVNVAACSPWCKTGGLGVAGALPKALARGHRVNVVPRYG 352
D 167 HYGMWILG-LGGEVNVNVIIVAACSPWCKTGGLGVAGALPKALARGHRVNVVPRYG 225
QY 353 DYEAVGVGRKTYKAAAGQDMEVNYFHAVIDGVDFVIDA.PLRHROED.YGSSROEIMK 412
D 226 DYVAEAFWGIKRYKAAAGQDLEVVYFHAVIDGVDFVIDAS-FRRHRODDIYGSSROEIMK 284
QY 413 RMILFCKAAVEVPMHVPFCGVPYDGNLVFIANDMHTALLPVYLKAYYRDHGLMOYTRSI 472
D 285 RMILFCKAAVEVPMHVPFCGVPYDGNLVFIANDMHTALLPVYLKAYYRDHGLMOYTRSV 344
QY 473 MYIHNIAHOGRGVDEPFTELEPHYLEHFRLYDPVGGEHANTFAA-GLKMDQVYVVP 531
D 345 LVHINIGHOGRGVDEPFTELEPHYLEHFRLYDPVGGEHANTFAA-GLKMDQVYVVP 404
QY 532 GYLWEIKTVGSGMGLHDIIRONDWKTGIVNGIDNMENPEVDYHLKSDGTNFSIGTLD 591
D 405 GYLWEIKTVGSGMGLHDIIRONDWKTGIVNGIDNMENPEVDYHLKSDGTNFSIGTLD 464
QY 592 SGKROCKEALQRELGLQVADVPILGFTIGLDGQKVEIADAMPWISODVOLVMLGTG 651
D 465 AGKROCKAALQRELGLQVADVPILGFTIGLDGQKVEIADAMPWISODVOLVMLGTG 524
QY 652 RHDLESMTLHFRERHHDKVRGNGVGSVRLAHRTAGADALLMPSEFPDGLNLYAMA 711
D 525 PDLERMLQHLERHHPNKVRGNGVGSVRLAHRTAGADALLMPSEFPDGLNLYAMA 583
QY 712 TVPVHAAGVGRDTPPDPFENHSGLGWTFPDAENKLIIEALGHCLTRYDDYKESWGLQ 771
D 584 TVPVHAAGVGRDTPPDPFENHSGLGWTFPDAENKLIIEALGHCLTRYDDYKESWGLQ 643
QY 772 ERGMSQDSFWEHAALYEDVLLKAYQW 799
D 644 ARGMSQNSMDHAAELYEDVLL-KYQW 669

RESULT 14
AAM70892

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ID AAM70892 standard; Protein; 804 AA.  
 XX AAM70892;  
 AC  
 XX 23-AUG-1999 (first entry)  
 DT  
 XX  
 DE Maize starch soluble synthase IIb.  
 XX  
 KM Non-glycogen-like polysaccharide production; fermentation;  
 KM starch synthase enzyme; glycogen-synthesis enzyme; glycogen synthesis;  
 KM non-starch branching gene; amylopectin; amylose; plant-like starch;  
 KM maize starch soluble synthase IIb.  
 XX  
 OS Zea mays.  
 XX  
 FN WO9844780-A1.  
 XX  
 PD 15-OCT-1998.  
 XX  
 PE 03-APR-1998; 98WO-US06660.  
 XX  
 PR 04-APR-1997; 97US-0042939.  
 XX  
 PA (EXSE-) EXSEED GENETICS LLC.  
 XX  
 PI Guan H, Keeling PL;  
 XX  
 DR WPI: 1998-568285/48.  
 DR N-PSDB; AAV70958.  
 XX  
 PT Producing non-glycogen-like polysaccharides in bacteria, fungi or  
 PT plants - transformed with genes for enzymes involved in starch or  
 PT glycogen synthesis allows fermentative production of starches with  
 PT engineered properties  
 XX  
 PS Disclosure; Fig 50; 150pp; English.  
 XX  
 CC The specification describes a method for the production of  
 CC non-glycogen-like polysaccharides in a host. The method comprises  
 CC transforming a host, suitable for fermentation, with genes encoding  
 CC starch- or glycogen-synthesis enzymes, and fermenting the transformants.  
 CC The specification also describes hosts transformed with a gene active  
 CC in glycogen synthesis and at least one non-starch branching gene,  
 CC involved in production of amylopectin or amylose in its original host.  
 CC The method is used to produce plant-like starches by fermentation and  
 CC new starches in plants. These starches are useful for all food and  
 CC non-food applications of starch. The present sequence is used in  
 CC the course of the invention.  
 XX  
 SQ Sequence 804 AA;  
 XX  
 Query Match 54.2%; Score 2319.5; DB 19; Length 804;  
 Best Local Similarity 58.0%; Pred. No. 8,6e-180;  
 Matches 469; Conservative 75; Mismatches 145; Indels 119; Gaps 15;

DB 164 -----VBS-----IGIAEPVDAKADAPATAAASAP 190  
 QY 293 H-HONEDSGPLAGNNVNVVVAECSPMCKIGLGDVAGALPKALAKGHRVMVVPY 351  
 DB 191 YREDNEPGLAGNNVNVVVAECSAPCKIGLGDVAGALPKALAKGHRVMVVPY 250  
 QY 352 GDYEADVGVKRYKKAAGODMEVNFHAYIIVDVFIDAPLFRHROEDYIGSSOEIM 411  
 DB 251 GEVAPADLGVRKRYKKAAGODSEVTFHAYIIVDVFIDAPLFRHROEDYIGSSOEIM 310  
 QY 412 KEMTLFCKAAVEVWVPCGGVPFGDENVFANDMTALLPYTKAYRDHGMOTRS 471  
 DB 311 KEMTLFCKAAVEVWVPCGGVFGDENVFANDMTALLPYTKAYRDHGMOTRS 370  
 QY 472 IMVHNINAGRGVDEFPFTELPEHYLEHRLYDPVGEHANYFAAGLRKADQVVVSP 531  
 DB 371 VLVHNINAGRGVDEFPFTELPEHYLEHRLYDPVGEHANYFAAGLRKADQVVVSP 430  
 QY 532 GYLMELKTVEGGKGLHDIIRONDPKRTGYNGIINDMEVNEVDVHLKSDGYNPSLGLTD 591  
 DB 431 GYLMELKTVEGGKGLHDIIRONDPKRTGYNGIINDMEVNEVDVHLKSDGYNPSLGLTD 490  
 QY 592 SGKQCKEALGREGLGVADVPPLGFTIGLDGQKVEIADAMPVIVSDVQVLMGTG 651  
 DB 491 TGRQCKAALORGLQVADVPPLGFTIGLDGQKVEIADAMPVIVSDVQVLMGTG 550  
 QY 652 RHDLSMLRPEREHDKVGVGSYVLAHRTAGDALIMPERFPCGLNOLYMAVG 711  
 DB 551 RADLEDMLRPEREHDKVGVGSYVLAHRTAGDALIMPERFPCGLNOLYMAVG 610  
 QY 712 TYPVHAAGVADVPFPDPFNHSGLGWTPDRAAHKLEALGHCLTYRYDKESWGLQ 771  
 DB 611 TYPVHAAGVADVPFPDPFNHSGLGWTPDRAAHKLEALGHCLTYRYDKESWGLQ 670  
 QY 772 ERGMSQDPSWEHAALYEDVILKAYQW 799  
 DB 671 ARGMAEDLSWDAALYEDVILKAYQW 698  
 RESULT 15  
 AAM56487  
 ID AAM56487 standard; Protein; 698 AA.  
 XX  
 AC AAM56487;  
 XX  
 DT 11-SEP-1998 (first entry)  
 XX  
 DE Zea mays soluble starch synthase IIb.  
 XX  
 KM SER; starch-encapsulating region; fusion vector;  
 KM soluble starch synthase IIb; glucosyl transferase.  
 XX  
 OS Zea mays.  
 XX  
 FN WO9814601-A1.  
 XX  
 PD 03-APR-1998.  
 XX  
 PE 30-SEP-1997; 97WO-US17555.  
 XX  
 PR 30-SEP-1996; 96US-0026855.  
 XX  
 PA (EXSE-) EXSEED GENETICS LLC.  
 XX  
 PI Guan H, Keeling P;  
 XX  
 DR WPI: 1998-240100/21.  
 DR N-PSDB; AAV29755.  
 XX  
 PT Hybrid polypeptide comprising starch-encapsulating region and  
 PT protein - useful for, e.g. producing protein(s) resistant to  
 PT degradation by stomach acids  
 XX

PS Example 2; Page 36-38; 156pp; English.

XX The sequence is that of soluble starch synthase IIb.  
 CC It can be used in the production of a hybrid polypeptide  
 CC comprising a starch-encapsulating region (SER) fused  
 CC to a payload protein. The hybrid polypeptide can be used to make  
 CC modified starches comprising the payload protein, selected from,  
 CC e.g. hormones, growth factors, antibodies, enzymes, dyes,  
 CC immunoglobulins, etc. The modified starch can also be used  
 CC to provide grain feeds enriched in amino acids. By encapsulating  
 CC the payload protein in starch, it is more resistant to  
 CC degradation by stomach acids.

XX Sequence 698 AA;

Query Match 54.1%; Score 2314.5; DB 19; Length 698;  
 Best Local Similarity 57.9%; Pred. No. 1.8e-179;  
 Matches 468; Conservative 76; Mismatches 145; Indels 119; Gaps 15;

QY 1 MSQVAGAGFLALASAPGSRRAVSA---PPHAGG-RLHMP-PMPQRTARDG 55  
 DB 1 MPQALISSSSAFLLFVASSSPRRRGSGALRSYGSGAELRLHMRGPQ---DGA 56  
 QY 56 VAAAPAGKQKRVDDDA---SARQPARRGATKVAERDDPVKTLDRDAEGAPAP 112  
 DB 57 ASVBAAPAGGSEBAKSSSSQAGAVGSTAKV-----DSAPPNPLTS 104  
 QY 113 APRODAARPPSWNGTPVNGENKSTGGGATYDGLPAPAPAPHPSTONRVVNGENKANY 172  
 DB 105 APKQ-----SQSAMQNG---TSGSSASATPAFVSGP-KADHPS----- 139  
 QY 173 ASPPTSLAEVAPDSATISIDKAPESVPAEKPPSPSGSNFVVSASAPRLDIDSDVEP 232  
 DB 140 -----AVTKKEIDAS-----AVKEPRAG-----DDAP 163  
 QY 233 ELKKGAVIVEBAPNPKALSPAPAPVOEDLWDFKKYIGFEEPVAKDDGNAVADAGSFE 292  
 DB 164 -----VES-----IGIAEPVDAAKADAAPATDAASAP 190  
 QY 293 H-HQNHDSGLAGENVVVVAAECSPWCKTGGIDVAGALPKALAKRGHVVVVVRY 351  
 DB 191 YDRENEBGPLAGPVMVNVVVASCAPCKTGGIDVAGALPKALAKRGHVVVVVRY 250  
 QY 352 GDYEAVYDVYKRYKKAAGDMEVNYFPAVYIDGVFVFIDAPLFRHQEDIYGGSRQEI 411  
 DB 251 GEYAEARLDGVRRYRYKVAQDSEVTFYHSYIDGVDFVFEAPPRHRNNIYGGSRDIL 310  
 QY 412 KRMILFCAAEVFNHVCVPGVDDGLVFIANDMHTALLPVYLKAYYRDHGLMOTRS 471  
 DB 311 KRMILFCAAEVFNHVCVPGVDDGLVFIANDMHTALLPVYLKAYYRDHGLMOTRS 370  
 QY 472 IMVINIAHOGGSPVDEFPTELPEHYLHEFLYDVPGEHANYPAAGLKXADQVVVVP 531  
 DB 371 VLVINIAHOGGSPVDEFPTELPEHYLHEFLYDVPGEHANYPAAGLKXADQVVVVP 430  
 QY 532 GYLMEKTVGGWGLHDIIRQNDKTRGIVNGIDMENVPEVDVHLKSDGYTNFSLGLTD 591  
 DB 431 GYMELKTVGGWGLHDIIRQNDKTRGIVNGIDMENVPEVDVHLKSDGYTNFSLGLTD 490  
 QY 592 SGKROCKALORELGIQVADVPILGFIGRLDGKVEIADAMPWIVSDVQLVMLGTG 651  
 DB 491 TSKROCKALORELGIQVADVPILGFIGRLDGKVEIADAMPWIVSDVQLVMLGTG 550  
 QY 652 RHDLSEMLRHFREHHDKYRGVGSVRLAHRITAGADALLMPSRFPCGINQIYAMAYG 711  
 DB 551 RADLEDMLRFESEHSDKRVAVGFSVPLAHRITAGADILMPSRFPCGINQIYAMAYG 610  
 QY 712 TVPVVHAAGVADTVPPDFPFHSGIWTFPDRAEAKLIEALGHCLFTYRDYKESWRGLQ 771  
 DB 611 TVPVVHAAGVADTVPPDFPFHSGIWTFPDRAEAKLIEALGHCLFTYRDYKESWRGLQ 670  
 QY 772 ERGMSQDPSWEHAALYEDVLLKAYQW 799

DB 671 ARGMAEDLSMDHAVALYEDVLLKAYQW 693

Search completed: February 20, 2004, 11:11:20  
 Job time : 51 secs

Mon Feb 23 11:51:13 2004

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Page 1

GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: February 20, 2004, 11:10:23 ; Search time 22 Seconds  
(without alignments)  
1536.653 Million cell updates/sec

Title: US-10-018-418-4

Sequence: 1 MSAAVASAFLALASASPC.....SWEHAKYEDVLTAKYQW 799

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/prodata/1/1aa/PCUTS\_COMB.pep:\*
- 6: /cgn2\_6/prodata/1/1aa/backfillseq1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4075	95.3	799	4	US-09-196-390-6
2	2432	56.9	669	3	US-08-941-445A-9
3	2314.5	54.1	698	3	US-08-941-445A-11
4	2163	50.6	801	4	US-09-388-743-26
5	2150.5	50.3	767	3	US-08-836-567-8
6	2150.5	50.3	767	4	US-09-606-304-8
7	2063	48.2	690	4	US-09-388-743-6
8	2059	48.2	558	4	US-08-836-567-6
9	2059	48.2	558	4	US-09-606-304-6
10	1201.5	28.1	649	4	US-09-192-909-2
11	1176	27.5	641	3	US-08-836-567-10
12	1176	27.5	641	4	US-09-606-304-10
13	1138.5	26.6	611	4	US-09-196-390-2
14	1066	24.9	583	3	US-08-941-445A-13
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16	1004.5	23.5	459	3	US-08-836-567-4
17	1004.5	23.5	459	4	US-09-606-304-4
18	907	21.2	616	4	US-09-388-743-14
19	885	20.7	615	4	US-09-388-743-2
20	869	20.3	533	3	US-08-941-445A-5
21	867	20.3	600	4	US-09-388-743-22
22	862	20.2	609	3	US-08-941-445A-7
23	841	19.7	614	4	US-09-388-743-18
24	599	14.0	477	1	US-07-735-065-2
25	599	14.0	477	1	US-08-469-202-12
26	599	14.0	477	2	US-08-484-434C-12
27	599	14.0	477	4	US-09-384-361-12

28	587.5	13.7	533	4	US-09-388-743-10	Sequence 10, Appl
29	572.5	13.4	735	3	US-09-115-704-2	Sequence 2, Appl
30	541	12.7	677	3	US-08-836-567-2	Sequence 2, Appl
31	541	12.7	677	4	US-09-606-304-2	Sequence 12, Appl
32	541	12.7	1197	3	US-08-836-567-12	Sequence 12, Appl
33	541	12.7	1197	4	US-09-606-304-12	Sequence 35, Appl
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36	490	11.5	549	4	US-09-252-991A-2468	Sequence 2468, A
37	415	9.7	476	4	US-09-198-452A-1021	Sequence 1021, Ap
38	178	4.2	64	2	US-08-470-720-15	Sequence 15, Appl
39	173.5	4.1	826	4	US-09-894-998A-47	Sequence 47, Appl
40	158.5	3.7	461	4	US-09-252-991A-24717	Sequence 24717, A
41	158	3.7	451	4	US-09-252-991A-27602	Sequence 27602, A
42	157.5	3.7	615	4	US-09-252-991A-25642	Sequence 25642, A
43	154.5	3.6	276	4	US-09-252-991A-23623	Sequence 23623, A
44	153.5	3.6	697	4	US-09-252-991A-24009	Sequence 24009, A
45	152	3.6	728	4	US-09-252-991A-31891	Sequence 31891, A

#### ALIGNMENTS

RESULT 1  
US-09-196-390-6  
Sequence 6, Application US/09196390  
Patent No. 6307125  
GENERAL INFORMATION:  
APPLICANT: Block, Martina  
APPLICANT: Lotz, Horst  
APPLICANT: Luticke, Stephanie  
APPLICANT: Walter, Lemart  
APPLICANT: Froberg, Claus  
APPLICANT: Kosmann, Jens  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES  
TITLE OF INVENTION: FROM WHEAT WHICH ARE INVOLVED IN STARCH  
NUMBER OF INVENTION: 9  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/196,390  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 196 21 588.9  
FILING DATE: 29-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 196 36 917.7  
FILING DATE: 11-SEP-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP97/02793  
FILING DATE: 28-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley, Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: AGREVO-9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 799 amino acids

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us-10-018-418-4.ra1

Page 2

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-196-390-6

Query Match 95.3%; Score 4075; DB 4; Length 799;  
Best Local Similarity 95.6%; Pred. No. 0;  
Matches 764; Conservative 7; Mismatches 28; Indels 0; Gaps 0;

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DB 61 AGKDAVDDDAASARPPRARGGAAATKVAERDDPKYTLDRDAEGGAPAPAPRODAR 120
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DB 121 PPSMNGTPVNGENKSTGGGATKDSGLPAPAPAPHPSTONRVNGENKXANVASPTSTA 180
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DB 181 EVAPDGAATISIDKAPESVYPAEKPPSSGGSFVVSASAPRLDIDSDVEPLKKGAVI 240
QY 181 EVAPDGAATISIDKAPESVYPAEKPPSSGGSFVVSASAPRLDIDSDVEPLKKGAVI 240
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QY 361 GVRKYVKAAGDMENVYFAIYDGVDFIDAPLFRROEDITYGSSQELMKMILFCKA 420
DB 361 GVRKYVKAAGDMENVYFAIYDGVDFIDAPLFRROEDITYGSSQELMKMILFCKA 420
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DB 421 AVEVPMVHPCGGVPGDGNLFIANDWHTALLPYLLKAYTRDGLMGTYSIMYINIAH 480
QY 481 QGRGVDFEPTTELPEHYLEHFLYDYPVGEHANYFAAGLKMADQVYVSSGYIMELKTV 540
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QY 541 EGGWGLMDIIRQNDWKTGRIYNGIDNMENPEVDVILKSDGYTNPSLGLDSGRCKEA 600
DB 541 EGGWGLMDIIRQNDWKTGRIYNGIDNMENPEVDVILKSDGYTNPSLGLDSGRCKEA 600
QY 541 EGGWGLMDIIRQNDWKTGRIYNGIDNMENPEVDVILKSDGYTNPSLGLDSGRCKEA 600
DB 541 EGGWGLMDIIRQNDWKTGRIYNGIDNMENPEVDVILKSDGYTNPSLGLDSGRCKEA 600
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DB 601 LQREGLQVADVPLLGFTIGRLDGQGYEIIADAMPVVSODVQVLMGLTGRHLEMLR 660
QY 601 LQREGLQVADVPLLGFTIGRLDGQGYEIIADAMPVVSODVQVLMGLTGRHLEMLR 660
DB 601 LQREGLQVADVPLLGFTIGRLDGQGYEIIADAMPVVSODVQVLMGLTGRHLEMLR 660
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DB 661 HFERHHDKVRGVMGFSVRLAHRTAGADALMPSEFCGJNOLYANAAYGVVAVAG 720
QY 661 HFERHHDKVRGVMGFSVRLAHRTAGADALMPSEFCGJNOLYANAAYGVVAVAG 720
DB 661 HFERHHDKVRGVMGFSVRLAHRTAGADALMPSEFCGJNOLYANAAYGVVAVAG 720
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DB 721 GYRDVVPFDPFNHSGLQWTPDRAHKLIEALGCLTYRDYKESWNGLOERMSODFS 780
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QY 781 WEHAAKLYEDVLKAKYQW 799
DB 781 WEHAAKLYEDVLKAKYQW 799
QY 799 WEHAAKLYEDVLKAKYQW 799
DB 799 WEHAAKLYEDVLKAKYQW 799
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TITLE OF INVENTION: Starch Encapsulation  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Circle  
CITY: Boulder  
STATE: CO  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/941,445A  
FILING DATE: 30-SEP-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026,855  
FILING DATE: 30-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Winner, Ellen P  
REGISTRATION NUMBER: 28,547  
REFERENCE/DOCKET NUMBER: 89-97  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8080  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 669 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-941-445A-9

Query Match 56.9%; Score 2432; DB 3; Length 669;  
Best Local Similarity 65.0%; Pred. No. 14e-214;  
Matches 466; Conservative 58; Mismatches 120; Indels 84; Gaps 12;

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DB 122 -----GIAPTYEPLVQEAITMDPKYIGFEEPEAKDDGMVAVDAGSFE 166
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DB 293 HHQNDHSGPLAENNVNVAACSPWCCTGGLDVGALPKALAKGHRMVMVVPYGY 352
QY 167 HYGTMILG-LGEBNVNVAACSPWCCTGGLDVGALPKALAKGHRMVMVVPYGY 225
DB 167 HYGTMILG-LGEBNVNVAACSPWCCTGGLDVGALPKALAKGHRMVMVVPYGY 225
QY 353 DYEADVGRKRYKAAAGDMENVYFAIYDGVDFIDAPLFRROEDITYGSSQELMK 412
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QY 226 DYEADVGRKRYKAAAGDMENVYFAIYDGVDFIDAPLFRROEDITYGSSQELMK 284
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QY 285 RMILFCKAAVEVPMHPCGGVPGDGNLFIANDWHTALLPYLLKAYTRDGLMGTYSI 344
DB 285 RMILFCKAAVEVPMHPCGGVPGDGNLFIANDWHTALLPYLLKAYTRDGLMGTYSI 344
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DB 473 MYHNTAAGRGVDFEPTTELPEHYLEHFLYDYPVGEHANYFAAGLKMADQVYVSS 531
QY 345 LVHNTIGHQGRGVHFPYMDLNTVLQHFHLYDYPVGEHANYFAAGLKMADQVYVSS 404
DB 345 LVHNTIGHQGRGVHFPYMDLNTVLQHFHLYDYPVGEHANYFAAGLKMADQVYVSS 404
QY 532 GYLMEIKTVGGWGLMDIIRQNDWKTGRIYNGIDNMENPEVDVILKSDGYTNPSLGLTD 591
DB 532 GYLMEIKTVGGWGLMDIIRQNDWKTGRIYNGIDNMENPEVDVILKSDGYTNPSLGLTD 591
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 DB 465 AGRCQCKAALQRDVGLVEDVDVPLIFIGLIDQCKGVDIIGDAMPVIAQDVQVLMGTG 524  
 QY 652 RHLESMLRHEERHHDKVRGWSVRLAHRITAGADALIMPSPREGCINQVLMAYG 711  
 DB 525 PDLERMLQLEHEHKNKRGWVFSVLMVHRITTPQASVLMPSRAG-GLNQLYMAVG 583  
 QY 712 TVPVHAGVGRDTPVPEFDPNHSGLGWTFRDAEAKLIEALGCLRTYRDYKESNRGLQ 771  
 DB 584 TVPVHAGVGRDTPVAFDPFGDGLGWTFRDAEANKLIEVLSHCLDTYRNYEESWKSQ 643  
 QY 772 ERGMSQPSWEHAKLYEDVILKAKYQW 799  
 DB 644 ARGMSQMLSMWHAELYEDVLV--KIQW 669

RESULT 3

US-08-941-445A-11  
 ; Sequence 11, Application US/08941445A  
 ; Patent No. 6107060  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Keeling, Peter  
 ; APPLICANT: Guan, Hanning  
 ; TITLE OF INVENTION: Starch Encapsulation  
 ; NUMBER OF SEQUENCES: 37  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
 ; STREET: 5370 Manhattan Circle  
 ; CITY: Boulder  
 ; STATE: CO  
 ; COUNTRY: US  
 ; ZIP: 80303  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/941,445A  
 ; FILING DATE: 30-SEP-1997  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/026,855  
 ; FILING DATE: 30-SEP-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Winner, Ellen P  
 ; REGISTRATION NUMBER: 28,547  
 ; REFERENCE/DOCKET NUMBER: 89-97  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (303) 499-8080  
 ; TELEFAX: (303) 499-8089  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 698 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-941-445A-11

Query Match 54.1%; Score 2314.5; DB 3; Length 698;  
 Best Local Similarity 57.9%; Pred. No. 9.2e-204;  
 Matches 468; Conservative 76; Mismatches 145; Indels 119; Gaps 15;

QY 1 MSAAVAAAGFLALASAPGRSRRARVSA---PPHAGAG-RHWP-PMPPORTADGG 55  
 DB 1 MPGAISSSSAFLFPVASSSPRRRGVGAALRSYGSGLRLHWRARGPQ---DGA 56  
 QY 56 VAAABAAGKADARVDDAA---SARQPRARRGGAATKVAERRDPVKTLDRAAEAGAPAP 112

DB 57 ASVRAAAAAPAGESEEAAKSSSSQAGAVOGSTAKAV-----DSAPPNPLTS 104  
 QY 113 APRODAAAPPSMNGTPTVNGENKSTGGGATKUSGLPAPAPAPSTONKRPVANGENKANY 172  
 DB 105 APKO-----SQSAMONG---TSQSSASTLAPEVSGP-RADHP----- 139  
 QY 173 ASPPTSAIEVAPDPAATISISDAPESVVPVUEKPPSSGSGNFVVASAPRLDIDSDVER 232  
 DB 140 -----APTCKEIDAS-----VYKPEBAG-----DDARP 163  
 QY 233 ELKKGAVIYEAAPNPKALSPAPAVOEDIMDFKTYGFEPEYBAKDDGMAVADAGSFE 292  
 DB 164 -----VES-----IGIAEPVAKADAAPATDAASAP 190  
 QY 293 H-HONHDSGLAGENNANVVVAACSPMCKTGGGLGVAGALPKALARGHRVYVVPXY 351  
 DB 191 YDRDNEGRPLAGPNNVNVVYVASECAPFCKTGLGIVGALPQALARRGHRVYVVPXY 250  
 QY 352 GDYEAADVGRKYKAAQDMENVYFAYIDGVFVITAPLFRHQEDIIYGSRCQEM 411  
 DB 251 GEYAEARDLGVRRRYKVAAGDSEVTFPHSYIDGVDFVEAPPRRHHNNIYGERLDIL 310  
 QY 412 KRMILFCKAAVEVPMHVPCGGVPGDGNLVEFANDMTALLPYLKAYYRDHGLMOTRS 471  
 DB 311 KRMILFCKAAVEVPMHVPCGGVPGDGNLVEFANDMTALLPYLKAYYRDHGLMOTRS 370  
 QY 472 IMVHNIAHOGRGVDEPFTELPEHYLEHFRUYDPVGEHANYFAAGLRKADQVVVVP 531  
 DB 371 VLVHNIAHOGRGVDEPFVNFEDLPEHYIDHFIQVDNIGCHSNVFAAGLTKADRVVTVSN 430  
 QY 532 GYIMELKTVGEGGLDIIIRNDWKTRGIYVIGDMNMBNBEVDVHLASDGTNYSLETTD 591  
 DB 431 GYIMELKTVGEGGLDIIIRNDWKTRGIYVIGDMNMBNBEVDVHLASDGTNYSLETTD 490  
 QY 592 SGRQCKEALQRELGLQVRAVPLLGIFGLDQCKVEIADAMPVISOVQVLMGTG 651  
 DB 491 TGRQCKAALQRLQGLQVRAVPLLGIFGLDQCKVEIADAMPVISOVQVLMGTG 550  
 QY 652 RHLESMLRHEERHHDKVRGWSVRLAHRITAGADALIMPSPREGCINQVLMAYG 711  
 DB 551 RADLEDMLRRESSESDVRAWVGSVRLAHRITAGADALIMPSPREGCINQVLMAYG 610  
 QY 712 TVPVHAGVGRDTPVPEFDPNHSGLGWTFRDAEAKLIEALGCLRTYRDYKESNRGLQ 771  
 DB 611 TVPVHAGVGRDTPVAFDPFGDGLGWTFRDAEANKLIEVLSHCLDTYRNYEESWKSQ 670  
 QY 772 ERGMSQPSWEHAKLYEDVILKAKYQW 799  
 DB 671 ARGMAEDLSMWAELYEDVLVYKAYQW 693

RESULT 4

US-09-388-743-26  
 ; Sequence 26, Application US/09388743  
 ; Patent No. 6423886  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Singletary, George  
 ; APPLICANT: Zhou, Ian  
 ; TITLE OF INVENTION: Use in the Production of New Starches  
 ; FILE REFERENCE: 1144  
 ; CURRENT APPLICATION NUMBER: US/09/388,743  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 26  
 ; LENGTH: 801  
 ; TYPE: PRT  
 ; ORGANISM: Typha latifolia  
 ; US-09-388-743-26

Query Match 50.6%; Score 2163; DB 4; Length 801;  
 Best Local Similarity 60.7%; Pred. No. 9.6e-190;

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us-10-018-418-4.ra1

Page 4

Matches 426; Conservative 84; Mismatches 151; Indels 41; Gaps 9;

QY 134 KSTGGGATKDSG--LPAPARHPSTORVRPVNGENKKNVAPSPSISAEVAPDSAAIT 191  
21 RATCKSGSEEESEEGEGRAGVGDALRATIDKNE--IAIHENLLOAKKNIVS 78

QY 192 SI-SDRAPE-----SVVPAEKPPSSG-----SNVYSA-- 219  
79 SIRSVDYKENDSSVYEKENLEPPSSGEONGKYSAGVANNYSQALQDDTSNPLPNSFG 138

QY 220 SARPLDSDVPEELKKGAVIVEAPNPKALSP--AAPVODLMDPKKYIGFEEPVYA 277  
139 GSPKDNVEA-VEFOVRSAVDAGRFEPSLGTTKILSPYILAEEDDAKERAEDLVA 197

QY 278 KDDGMAVADAGSEFHQNDHSGPLAGENVVNVVVAECSPWCKTGSLGVAGALPKAL 337  
198 KLDGVHKDLDNPGE--ENEVPLPLAGANNVNIIVAAECAPWSKTGGLGVAGALPKAL 255

QY 338 AKRGHRVNVVPRYGVDEEAYDVGKYYKAGODMEVNFHAYIDGVDFVFLDAPLEH 397  
256 ARRGHRVNVVPRYGVDEEAYDVGKYYKAGODMEVNFHAYIDGVDFVFLDAPLEH 315

QY 398 ROEDYGGSGROEIMKEMILFCKAAVEVPMHVPCCGVVPGDGLVFLANDMHTALLPVYLK 457  
316 RGRNRYEGRNVLDILKRMILFCKAAVEVPMHVPCCGVVPGDGLVFLANDMHTALLPVYLK 375

QY 458 AAYRDHGLMOTYSIMVTHIAHQGRPNDEFFTLPEHYLEHFLYDPVGEHANVYA 517  
376 AAYRDHGLMOTYSIMVTHIAHQGRPNDEFFTLPEHYLEHFLYDPVGEHANVYA 435

QY 518 AGLMADQVNVVSPGYLMEIKTVEGSGWGLHDIIRQNDMKRGLVINGIDNMENNEVYVHL 577  
436 AGLMADQVNVVSPGYLMEIKTVEGSGWGLHDIIRQNDMKRGLVINGIDNMENNEVYVHL 495

QY 578 KSDGYTNSLGTLDGSGRCKEALQRELGLOPADVPLGFLGRLDGQGVETILANMWM 637  
496 KSDGYTNSLGTLDGSGRCKEALQRELGLOPADVPLGFLGRLDGQGVETILANMWM 555

QY 638 IVSODVOTVNLGTRHDLSEMLRFEERHDKVSGWVGFVRLAHLITAGADALLMPSRF 697  
556 IVSODVOTVNLGTRHDLSEMLRFEERHDKVSGWVGFVRLAHLITAGADALLMPSRF 615

QY 698 EPCGLNOLYAMAYGTIVVAVHAGVGRDTPPEPFNHSIGLGTFFDAEAKLIEALGHCL 757  
616 EPCGLNOLYAMAYGTIVVAVHAGVGRDTPPEPFNHSIGLGTFFDAEAKLIEALGHCL 675

QY 758 RTYRDYKESWRNGLOERGSODFSWEHAKLYEDVILKAKYQW 799  
676 RTYRDYKESWRNGLOERGSODFSWEHAKLYEDVILKAKYQW 717

RESULT 5  
US-08-836-567-8  
Sequence 8, Application US/08836567  
Patent No. 6130367  
GENERAL INFORMATION:  
Applicant: Kosseman, Jens  
Applicant: Springer, Franziska  
Applicant: Abel, Gernot  
TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES  
TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC  
TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSES: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDICAL TYPE: floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,567  
FILING DATE: 24-JUL-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP95/04415  
FILING DATE: 09-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 44 41 408.0  
FILING DATE: 10-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
TELEPHONE/DOCKET NUMBER: Agrevo-4  
TELEPHONE: 212-596-9090  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 767 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-836-567-8

Query Match 50.3%; Score 2150.5; DB 3; Length 767;  
Best local similarity 54.3%; Pred No. 1.3e-188; Indels 67; Gaps 10;  
Matches 426; Conservative 104; Mismatches 188;

QY 34 HAGAGRLHMPPEPQRTARPDGVAARAAGKDAVDDDAASAPQARRAGAAITKAERR 93  
31 HGSSEGVKWKIRKVAIGENSGEASADESNDA-LQVTEIKSKVYLMQODLLQOIAERR 89

QY 94 DPVYTLDRDA-----EGARA-----PPAPQDARAPSPNNGTPVNGENKSTGGGA 141  
90 KVSISIKSLNNAKGYDGGSLSDVDIPDVKDYNVYPTATITVDKNT----- 144

QY 142 TKDSGLPAPARAPSTONRVPVNGENKANYA---SPPTIAEVVADSAATISISXAP 198  
145 -----PAISODFVESKREIKRDLADRABPLRSISITA--SSQISSVSSKRT 191

QY 199 ESVVPAEKPPSSSGSNFVYSASAPRLDID-----SDVEPELKKGAVIVEAPNPKALSPA 254  
192 LN-VPEPFPKSSQETLDVNSRKSLLVDPGKKTOSYMPSLKSSASHVEORENLESGS 250

QY 255 APAVOEDLMDPKKYIGFEEPEYEAKDQAVAVADAGSEFHQNDHSGPLAGENVVNVVYA 314  
251 AEAENET-----EDPNI-----DEKPPPLAGTNVNIILVA 282

QY 315 AEGSPWCTGGLGVYAGALPKALAKRGHNVVVPYGVDEEAYDVGKYYKAAQDME 374  
283 SECAPWSKTGGLGVYAGALPKALAKRGHNVVVPYGVDEEAYDVGKYYKAAQDME 342

QY 375 VNYFAAYIDGVDFEVIDAPLFRHROEDYGG3ROEIMKMLFCKAAVEVPMHVPCCGVP 434  
343 VNYFAAYIDGVDFEVIDAPLFRHROEDYGG3ROEIMKMLFCKAAVEVPMHVPCCGVP 402

QY 435 YDDGNLVFIANDMHTALLPVYLKAYRPHGLKQTRBSIMVTHIAHQGRGVDEFFTEL 494  
403 YDDGNLVFIANDMHTALLPVYLKAYRPHGLKQTRBSIMVTHIAHQGRGVDEFFTEL 462

QY 495 PEHYLEHFLYDPVGEHANVYFAGLKAADQVNVVSPGYLMEIKTVEGSGWGLHDIIRND 554  
463 PEHYLEHFLYDPVGEHANVYFAGLKAADQVNVVSPGYLMEIKTVEGSGWGLHDIIRND 522

QY 555 WTRGIVNGIDNMENNEVYVHAKSDGYTNSLGTLDGSGRCKEALQRELGLOPADV 614  
523 WTRGIVNGIDNMENNEVYVHAKSDGYTNSLGTLDGSGRCKEALQRELGLOPADV 582

QY 615 LIGFGRLDGQGVETILANMWMYVSDVQVLMGTGHHDLSEMLRFEERHDKVGRGV 674  
615 LIGFGRLDGQGVETILANMWMYVSDVQVLMGTGHHDLSEMLRFEERHDKVGRGV 674

Db 583 LIFGIGRLDPQKVDLIAEASAMMGQDVQVLMGTGRDLQOMLROFECQNDKIRGW 642  
QY 675 GFSVRLAHRITAGADALLMPSPFCGLNQLYAMAYGVVAVGVADTVPPDPFNH 734  
Db 643 GFSVTSRITAGADILLMPSPFCGLNQLYAMAYGVVAVGVADTVPPDPFNH 702  
QY 735 SGLGTFPRARAHILALGNCCLTYRKYKSMGIGTROMTODLSMDNAQYEEVILIA 794  
Db 703 SGLGTFPRARASQILHALGNCCLTYRKYKSMGIGTROMTODLSMDNAQYEEVILIA 762  
QY 795 AKYQW 799  
Db 763 AKYQW 767

RESULT 6  
US-09-606-304-8  
Sequence 8, Application US/09606304  
Patent No. 6483010  
GENERAL INFORMATION:  
APPLICANT: Kossmann, Jens  
Springer, Franziska  
Abel, Gernot  
TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES  
INVOLVED IN STARCH SYNTHESIS IN TRANSGENIC  
PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/606,304  
FILING DATE: 28-Jun-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/836,567  
FILING DATE: <Unknown>  
APPLICATION NUMBER: DE P 44 41 408.0  
FILING DATE: 10-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: Agrevo-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 767 amino acids  
TYPE: amino acid  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-606-304-8

Query Match 50.3%; Score 2150.5; DB 4; Length 767;  
Best Local Similarity 54.3%; Pred. No. 1,3e-188; Indels 67; Gaps 10;  
Matches 426; Conservative 104; Mismatches 189; Indels 67; Gaps 10;  
QY 34 HAGAGRLHWPWPQRTARQGVAAARAGKDAVDDAASARQPARRGAATKVAER 93  
Db 31 HGSRRQGMWTKRKVKATGENSGEASADENSNDALQVTKISKVKVLAHQDILLQIAER 89  
QY 94 DPVYTLDRDA-----EGGARA-----PPARQDAARPPSNVNGPYNKENSITGGGA 141

Db 90 KVVSSIKSLNNAKITYDGGSGSLSDVDLIDVDNDVNVTVFTRAAFLITVDKNT----- 144  
QY 142 TKDSGLPAPAPAPRPTSTQNVNPNVNGENKANA---SEPTSLAEVAPDSATISIDKAP 198  
Db 145 -----PPAISQDFVESKRRIKRDLDERAPPLSRSSITA-SQISSVSSKRT 191  
QY 139 ESVVPAKRPSSSSNNVVASAPRLID-----SDVEPELKGAAYIEEAPNKALSPPA 254  
Db 192 LN-VPEPFPSSQFTLLDVNSRKSLLVVPKGTQSTYPSLKSSASASHVEQRNLEGS 250  
QY 255 APAVOEDLMPFKKTYIGFEEPEVPEAKDDGMAVADAGSFEEHQNDSGPLAGENVANVVVA 314  
Db 251 AEANEET-----EDPVNI-----DEKPPPLAGTNVNIILVA 282  
QY 315 AEGSPWCKTGGLGVAGALPKALAKGRHVMVYVRYGDYEAVDVGVRYKYAAAGDME 374  
Db 263 SECAPWSKTKGLGVAGALPKALAKGRHVMVYVRYGDYEAVDVGVRYKYKYVGDVE 342  
QY 375 VNYFPAAYIDGVDVYFIDAPLFRHROEDYGGSSROEIKEMILPCKAAVEVPMVPCGGVP 434  
Db 343 VTYFOAFIDGVDVYFIDSHMFRHIGNNIYGSNRVDLKNRVLFPCKALIEVPMVPCGGVC 402  
QY 435 YGDNVFIANDMTALLPYLYKAYRDHGLMOYTRSIMYIHNIAHQGRGVDEFPTEL 494  
Db 403 YGDNVFIANDMTALLPYLYKAYRDHGLMOYTRSIMYIHNIAHQGRGVDEFPTEL 462  
QY 495 PEYLYHEPRLYDVPVGEHANVFAAGLKMADOVWVVSGLVMEKTYEGGGLHDIIKND 554  
Db 463 PPHYMDPFLYDVPVGEHANVFAAGLKMADOVWVVSGLVMEKTYEGGGLHDIIKND 522  
QY 555 WTRNGIVNGIDNMENPEVDVHLKSDGYTFPSLGTLDGKQCKEALQRELGLOVRADV 614  
Db 523 WKLQIVGVGIDTKEWNPBLDVHLQSDGYMNYSLDTLTGTGKQCKEALQRELGLOVRADV 582  
QY 615 LIGFGRGLDPQKVEIILADAMPVVSQDVOLVMTGRHDLSEVLRHFEERHDKYRW 674  
Db 583 LIGFGRGLDPQKVDLIAEASAMMGQDVQVLMGTGRDLQOMLROFECQNDKIRGW 642  
QY 675 GFSVRLAHRITAGADALLMPSPFCGLNQLYAMAYGVVAVGVADTVPPDPFNH 734  
Db 643 GFSVTSRITAGADILLMPSPFCGLNQLYAMAYGVVAVGVADTVPPDPFNH 702  
QY 735 SGLGTFPRARAHILALGNCCLTYRKYKSMGIGTROMTODLSMDNAQYEEVILIA 794  
Db 703 SGLGTFPRARASQILHALGNCCLTYRKYKSMGIGTROMTODLSMDNAQYEEVILIA 762  
QY 795 AKYQW 799  
Db 763 AKYQW 767

RESULT 7  
US-09-388-743-6  
Sequence 6, Application US/09388743  
Patent No. 6423886  
GENERAL INFORMATION:  
APPLICANT: Singletary, George  
APPLICANT: Zhou, Jian  
TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and Their  
FILE REFERENCE: 1144  
CURRENT APPLICATION NUMBER: US/09/388,743  
CURRENT FILING DATE: 1999-09-02  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 690  
TYPE: PRT  
ORGANISM: Curcuma zedoaria  
US-09-388-743-6

Query Match 48.2%; Score 2063; DB 4; Length 690;



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Page 6

Best Local Similarity 56.0%; Pred. No. 1,2e-180;

Matches 404; Conservative 80; Mismatches 166; Indels 72; Gaps 9;

QY 109 PABPAP-----RQDAPR---PAMNCTPVNGENKSTGGGATKYDGL-----BAP 150  
10 PABPPPGASCRLLHGAPBLGHSPLCMANPLCTSRFAGLSEVKKSGXITLKHIDTGS 69  
QY 151 AARP-----HSTQNRVPVNGENKANYASPTSTIAEVVAPDSATISIDSKAESVVP 203  
70 ARMRRLMALYHQSADLPVFNHGRSSGAVGNSIND-IQDSNDVDIADDSVAQIME 128  
QY 204 AEXPPSSGSNFVVSASAPRLDIDSDVEPELKKG-----AVTEAPNPKLSPAPAA 257  
129 QSKVLEMQNLLOQLIEKR-NFSEETESYKKDEMIGIYAEAYMQTSNNQOEAP----- 183  
QY 258 VQEDLMDFKYIGFEEVEAKDGMVADAGSFHHQNHDSGLPGENVAVVVAAC 317  
184 -----EAG-----NNSPPLGPRVNAIILVAAAC 208  
QY 318 SPWCKTGLGDVAGALPKALAKGHRVWVVPYGYEAYDVVGRKYKAAAGDMENVY 377  
209 APMSKIGLDVYGALPKALAKGHRVWVSPRYGNPEPKEIGNLKYKVDGQDWEIKY 268  
QY 378 FHAYIDGVDFIDAPLFRHROBDIYGSROEIMKMLFECKAAVPMHVPCCGVPYGD 437  
269 YHTYIDVDFVFDSPFRHIGNDIYGNRVDLKRWVLECKAAVEPMHVPCCGVPYGD 328  
QY 438 GNLVFIANDMHTALLPYLKAYYRDHGLMQYRSIMVINHIAHQGRGVDEFPTELPER 497  
329 GNLVFIANDMHTALLPYLKACFRDRLMTYARCLVTHINIAHQGRGLDPSYVDLPD 388  
QY 498 YLEHFRLYDPVGSNANYFAAGLKMADQVYVVSIGYIMELKYEGGGLHDIIRQNDWKT 557  
389 HIDEFRLLDDPVGSGHFPIFAAGIRADRVTVSHGVAMELKEGGLHEIINEGWF 448  
QY 558 RGIYNGIDNMENNEVDVHLKSDGYTNFSLGTLDSGRQCKEALQRELGQVADVPILG 617  
449 HGTYNGIDTHSNKPKFAHNSDGYTNFLETLEMGACCAALQREFGLPVDDVYILA 508  
QY 618 FIGRDLGQKYEIADAMPVYSQVQVLMGTRHLESMRFRFEHNDIKRGWVGS 677  
509 FIGRDLGQKIDILAEAMHMLVQDLOIMGTGRPLEDLRFRFEHNGKRGWVGS 568  
QY 678 VRLARITAGADALIMPFRFCGLOLYAMAAGTVPVHAGVGRVTPFPFNHSL 737  
569 VKMARITAGADALIMPFRFCGLOLYAMAAGTVPVHAGVGRVTPFPFNHSL 628  
QY 738 GWTEDRAAKLIEALHGLRTYRDYKESWEGLOERGSQDPSHEAAKLYEDVLLKAY 797  
629 GWTEDRAAHMIVALHGLNTYRKYKESWGLQKRGMMODLSWESAHEKVLVAKY 688  
QY 798 QW 799  
689 QW 690

RESULT 8

US-08-836-567-6

Sequence 6, Application us/08836567

Patent No. 6130367

GENERAL INFORMATION:

APPLICANT: Kosemann, Jens

APPLICANT: Springer, Franziska

TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES

TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC

TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESS: FISH & NEAVE

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836,567

FILING DATE: 24-JUL-1997

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/04415

FILING DATE: 09-NOV-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 41 408.0

FILING DATE: 10-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James P.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: Agrevo-4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-596-9000

TELEFAX: 212-596-9090

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 558 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-836-567-6

Query Match 48.2%; Score 2059; DB 3; Length 558;

Best Local Similarity 73.7%; Pred. No. 1.9e-180;

Matches 368; Conservative 62; Mismatches 69; Indels 0; Gaps 0;

QY 301 PLAGNNVAVVVAACEGPKCTGGLGVNAGLAKLAKRHRVWVVPYGYDEEAYDV 360  
60 PLAGNNVAVVVAACEGPKCTGGLGVNAGLAKLAKRHRVWVVPYGYDEEAYDV 119  
DB 60 PLAGNNVAVVVAACEGPKCTGGLGVNAGLAKLAKRHRVWVVPYGYDEEAYDV 119  
QY 361 GVRKYKXAGDMENVYFAYIDGVDFVFDAPLFRHROBDIYGSROEIMKMLFECKA 420  
120 GVRKYKXAGDMENVYFAYIDGVDFVFDAPLFRHROBDIYGSROEIMKMLFECKA 179  
QY 421 AVEVPMHVPCCGVPYGDNLVFIANDMHTALLPYLKAYYRDHGLMQYRSIMVINHIAH 480  
180 AVEVPMHVPCCGVPYGDNLVFIANDMHTALLPYLKAYYRDHGLMQYRSIMVINHIAH 239  
DB 180 AVEVPMHVPCCGVPYGDNLVFIANDMHTALLPYLKAYYRDHGLMQYRSIMVINHIAH 239  
QY 481 QGRGVDEFPTELPEHYLEHFRLYDPVGEHANYFAAGLKMADQVYVVSIGYIMELKTV 540  
240 QGRGVDEFPTELPEHYLEHFRLYDPVGEHANYFAAGLKMADQVYVVSIGYIMELKTV 299  
DB 240 QGRGVDEFPTELPEHYLEHFRLYDPVGEHANYFAAGLKMADQVYVVSIGYIMELKTV 299  
QY 541 EGGMGILHDIIRQNDWKTGRIVNGIDNMENNEVDVHLKSDGYTNFSLGTLDSGRQCKEA 600  
300 EGGMGILHDIIRQNDWKTGRIVNGIDNMENNEVDVHLKSDGYTNFSLGTLDSGRQCKEA 359  
DB 300 EGGMGILHDIIRQNDWKTGRIVNGIDNMENNEVDVHLKSDGYTNFSLGTLDSGRQCKEA 359  
QY 601 LQRELGQVADVPILGFTIGRDLGQKYEIADAMPVYSQVQVLMGTRHLESMRFRFEHNDIKRGWVGS 660  
360 LQRELGQVADVPILGFTIGRDLGQKYEIADAMPVYSQVQVLMGTRHLESMRFRFEHNDIKRGWVGS 419  
DB 360 LQRELGQVADVPILGFTIGRDLGQKYEIADAMPVYSQVQVLMGTRHLESMRFRFEHNDIKRGWVGS 419  
QY 420 QFECQNDKIRGVGSVTSRITAGADILIMPFRFCGLOLYAMAAGTVPVHAGVGRVTPFPFNHSL 479  
661 HFERHNDIKRGWVGSVTSRITAGADILIMPFRFCGLOLYAMAAGTVPVHAGVGRVTPFPFNHSL 720  
DB 420 QFECQNDKIRGVGSVTSRITAGADILIMPFRFCGLOLYAMAAGTVPVHAGVGRVTPFPFNHSL 479  
QY 721 GVRDYTPFPFNHSLGWTEDRAAKLIEALHGLRTYRDYKESWEGLOERGSQDPSHEAAKLYEDVLLKAY 780  
480 GVRDYTPFPFNHSLGWTEDRAAKLIEALHGLRTYRDYKESWEGLOERGSQDPSHEAAKLYEDVLLKAY 539  
DB 721 GVRDYTPFPFNHSLGWTEDRAAKLIEALHGLRTYRDYKESWEGLOERGSQDPSHEAAKLYEDVLLKAY 539  
QY 781 WEHAAKLYEDVLLKAYQW 799  
540 WEHAAKLYEDVLLKAYQW 558  
DB 781 WEHAAKLYEDVLLKAYQW 799  
540 WEHAAKLYEDVLLKAYQW 558

```

1      RESULT 9
2      US-09-606-304-6
3      ; Sequence 6, Application US/09606304
4      ; Patent NO. 6483010
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Kossmann, Jens
7      ;                Springer, Franziska
8      ;                Abel, Gernot
9      ; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
10     ; INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
11     ; PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
12
13     NUMBER OF SEQUENCES: 17
14     CORRESPONDENCE ADDRESS:
15     ADDRESSEE: FISH & NEAVE
16     STREET: 1251 Avenue of the Americas
17     CITY: New York
18     STATE: New York
19     COUNTRY: USA
20     ZIP: 10020
21
22     COMPUTER READABLE FORM:
23     MEDIUM TYPE: Floppy disk
24     COMPUTER: IBM PC compatible
25     OPERATING SYSTEM: PC-DOS/MS-DOS
26     SOFTWARE: Patentin Release #1.0, Version #1.30
27
28     CURRENT APPLICATION DATA:
29     APPLICATION NUMBER: US/09/606,304
30     FILING DATE: 28-Jun-2000
31     CLASSIFICATION: <Unknown>
32
33     PRIOR APPLICATION DATA:
34     APPLICATION NUMBER: 08/836,567
35     FILING DATE: <Unknown>
36     APPLICATION NUMBER: DE P 44 41 408.0
37     FILING DATE: 10-NOV-1994
38
39     ATTORNEY/AGENT INFORMATION:
40     NAME: Haley Jr., James F.
41     REGISTRATION NUMBER: 27,794
42     REFERENCE/DOCKET NUMBER: Agrevo-4
43
44     TELECOMMUNICATION INFORMATION:
45     TELEPHONE: 212-596-9000
46     TELEFAX: 212-596-9050
47
48     INFORMATION FOR SEQ ID NO: 6:
49     SEQUENCE CHARACTERISTICS:
50     LENGTH: 558 amino acids
51     TYPE: amino acid
52     TOPOLOGY: linear
53
54     MOLECULE TYPE: protein
55     SEQUENCE DESCRIPTION: SEQ ID NO: 6:
56     US-09-606-304-6

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[illegible]

Qy	601	LOBELSLQVRAVPLILGFGRIIDGGKGEVITADAMPINIVSODVUWLGGRIDLESMLR	663
Db	360	LQLELSLPVRDDVPLIGFGRIDPOKGVDLINEMSAMMGQDVUWVLTGGRDLEQMLR	419
Qy	661	HFEREHDDVVRGWSVGYRLAHRITAGADALI,MSRPEPCGLNLYAMAYGVTPVVAVG	720
Db	420	QFECQNDKIRGMVGSVYKTSHRITAGADIL,MSRPEALNLTVMKGTIPVVAVG	479
Qy	721	GVADIVPVPDPFNHSGLGWTFPDAAHKLIZLHGCHLRTDYVESNRGLQERMSQDFS	780
Db	480	GLRDTVQPPDPFNESGLGWTFRFAASOLIHVLGNCLLYREYKWSWEGIQTRCMTDLS	539
Qy	781	WEHAALVDEVLLAKAYQK	799
Db	540	WDNAQNVEEVLIAAYQK	558

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1      RESULT 10
2      US-09-192-909-2
3      / Sequence 2, Application US/09192909
4      / Patent No. 6307124
5      / GENERAL INFORMATION:
6      / APPLICANT: Jens Kossmann
7      / APPLICANT: Claus Froberg
8      / TITLE OF INVENTION: Nucleic acid molecules encoding soluble
9      / TITLE OF INVENTION: starch synthases from maize
10     / NUMBER OF SEQUENCES: 3
11     / CORRESPONDENCE ADDRESS:
12     / ADDRESSEE: James F. Haley, Jr., c/o FISH & NEAVE
13     / STREET: 1251 Avenue of the Americas
14     / CITY: New York
15     / STATE: New York
16     / COUNTRY: USA
17     / ZIP: 10020
18     / COMPUTER READABLE FORM:
19     / MEDIUM TYPE: Floppy disk
20     / COMPUTER: IBM PC compatible
21     / OPERATING SYSTEM: PC-DOS/MS-DOS
22     / SOFTWARE: Patentin Release #1.0, Version #1.30 (EPA)
23     / CURRENT APPLICATION DATA:
24     / APPLICATION NUMBER: US/09/192,909
25     / FILING DATE:
26     / CLASSIFICATION:
27     / PRIOR APPLICATION DATA:
28     / APPLICATION NUMBER: PCT/EP97/02527
29     / FILING DATE: 16-MAY-1997
30     / PRIOR APPLICATION DATA:
31     / APPLICATION NUMBER: DE 196 19 918.2
32     / FILING DATE: 17-MAY-1996
33     / ATTORNEY/AGENT INFORMATION:
34     / NAME: Haley, Jr., James F.
35     / REGISTRATION NUMBER: 27,794
36     / REFERENCE/DOCKET NUMBER: GFB-9
37     / TELECOMMUNICATION INFORMATION:
38     / TELEPHONE: 212-596-9000
39     / TELEFAX: 212-96-9090
40     / INFORMATION FOR SEQ ID NO: 2:
41     / SEQUENCE CHARACTERISTICS:
42     / LENGTH: 649 amino acids
43     / TYPE: amino acid
44     / TOPOLOGY: linear
45     / MOLECULE TYPE: protein
46     / US-09-192-909-2

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Query Match	28.1%	Score 1201.5	DB 4	Length 669
Beech Local Similarity	41.1%	Pred. No. 1-6e-101		
Matches	271	Conservative 86	Mismatches 210	Indels 93 Gaps 15
QY	176	FTSLAEVAVDPDAATISIDKAPSSVYPAAEK--PPSSGGNFVASAPRLDIDSVEPELK	235	
Dd	38	PRRQRYLRRRCVAELSRSGPAPRPMPLALAP-	71	
QY	236	KGAIVIEEAPRPKKLSPPAAPAVEDLDWDFKKYIGTFEPYEAKDDGMAVAD-----DAG	289	

Mon Feb 23 11:51:13 2004

us-10-018-418-4.trai

Page 8

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Db      72  -----LV-----PGLAPPAEPTGERPAL-----TTPPPVADAGLVGVPEEGSIAGB 112
Qy      290 SFEE-----HQNHDGCPAGEN-----VNVVVVVAACSPMCKTGIGLVAGALPYALAK 339
Db      113 SIDNTVVASQDEIIVGKEQARAKYTONIVFPTGASVYASGGIGDVCGSLPVALLA 172
Qy      340 RGRHVTVVPRY-----GDYEAVDGVRKYRYAAGDMENYFHAIVGVDVPTIDAP 393
Db      173 RGRHVTVVPRYLVNGTSDKRYANAFYTEKILIRPCFGHEHVFTHFHYRDSVMVWVDHP 232
Qy      394 LFRHROEDYV-----GSRQEIKMRLIFCKAAVEVPMVHPVCGVYDGNLVFLANDHTA 450
Db      223 SY-HRPGNLVGDKGFAPGDNQFRYTLDCYAACEAPLVLELGYTGO-NCMFVYNDWHAS 290
Qy      451 LIPVYLKAYYRDHGLMOTRSIMVTHNIAHOGRGPDVDEPPTPELPEHYL-----EHF 502
Db      291 LVPVLLAKYRPPYKDSRSILVHNLAHQGVPEASTYDPLGLPPEWYGALEWVPEWA 350
Qy      503 RLYDPVGGEHANYFAAGLKMADQVYVVSPPYLMELKTYEGSGMLHDIIRQNDWKTRGVN 562
Db      351 RRHALDKGAVNPLKGAIVVTAADRVTVYSKYSWEVTTAEQGGIENELSSRKSXTANGIVN 410
Qy      563 GIDNNENPVEDVHLKSDYTNFSLGTLDSGRCKCKEALQRELGQVRADVPLLGFTGRL 622
Db      411 GIDINDMNPATDKCIP-----CHYSVDL-SGKAKCKALQKELGLPIRPDVPILGFTGRL 465
Qy      623 DGQKVEIILADAMPVVSQDVOLVMTGGRHDLSEMLRHERHNDVVRGNGVSPVLAH 682
Db      466 DYQKIDIDLOIIPLMKREDVQFVVLGSDPELDMKSTBSIKDPRFGVGFVSUVAH 525
Qy      683 RITGADALLMPSPREPCGILNOLYAMAYGIVPVYHAGVADIVPPDPFNHS---GLGW 739
Db      526 RITGACDILMPSPREPCGILNOLYAMQYGVVYHATGGLADVENTENPFCENGEOGTGW 585
Qy      740 TEDRAEAKLLEALGHCHRTYRDYKESRGLOERGQODPSFMEAAALYEDVLLKAKYOM 799
Db      586 AFAPIITENMLTJLTAISTYREHKSWEGLMKRGMKDPFTWDAHQEYEOI-----FQW 640

RESULT 11
US-08-836-567-10
; Sequence 10, Application US/08836567
; Patent No. 6130367
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; APPLICANT: Springer, Franziska
; APPLICANT: Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,567
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04415
; FILING DATE: 09-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 41 408.0
```

```

; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Agrevo-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 641 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-836-567-10

Query Match      27.5%; Score 1176; DB 3; Length 641;
Best Local Similarity 45.2%; Pred. No. 3,4e-99;
Matches 250; Conservative 72; Mismatches 181; Indels 50; Gaps 12;

Qy      283 AYADAGSPFHQ--NHDGCPAGEN-----VNVVVVVAACSPMCKTGIGLVAG 330
Db      94 SVAGDATTWESHDIYANDRDLSDEPTMEETPIKLTFTNIIFTVRAAPYKTKGIGLVG 153
Qy      331 GALPVALAKRGRHVNVVPRY-----GDYEAVDGVRKYRYAAGDMENYFHAIVD 383
Db      154 GSLPVALAKRGRHVNVVPRYLVNGTSDKRYANAFYTEKILIRPCFGHEHVFTHFHYR 213
Qy      384 GVDVFEIAPLFRH---RQEDYV--GSRQEIKMRLIFCKAAVEVPMVHPVCGVYDGDG 438
Db      214 GVDWVFVDHSSYCRGTGYGDIYGAFGDNQ---FRFTLSHACAPLVLDGFTTGE- 269
Qy      439 NLVFLANDMHTALLPVYLKAYYRDHGLMOTRSIMVTHNIAHOGRGPDVDEPPTPELPEHY 498
Db      270 KCLFLANDMHTALLPVLLAAKRPYGVYKDSRIYAHNIAHOGVPAVYNNILGLPQW 329
Qy      499 LHFRLIYDPV-----GGEHANYFAAGLKMADQVYVVSPPYLMELKTYEGSGMLHDI 550
Db      330 YGAVENIPEPTWAKRALDGTETVNLKALIAVADRLIVSGYSNEITTPSGGIGLHLL 389
Qy      551 RQNDWKTRGVIVGIDNMEMNPEVDVHLKSDYTNFSLGTLDSGRCKCKEALQRELGQVR 610
Db      390 SSRQSVANGINTNGIDVNMWNPSTDEHIAS---HYSINDL-SGKVCCKTDQKEIGLPIR 444
Qy      611 ADVPLLGFTGRDQKGYEITLADAMPVVSQDVOLVMTGGRHDLSEMLRHERHNDVVR 670
Db      445 PCCPLIGFTGRDYGKGVDIILISALPELMQNDVQVVMGSEKQYEDMWRHTENLFDKXF 504
Qy      671 RQWGFVSVALRITAGADALLMPSPREPCGILNOLYAMAYGIVPVYHAGVADIVPPDP 730
Db      505 RAVGGRNVVSHRIIAGCDILMPSPREPCGILNOLYARIGTIPVHSTGGRLDTVKQFN 564
Qy      731 PFNHSGL---GWTDRRAEAKLLEALGHCHRTYRDYKESRGLOERGQODPSFMEAAK 786
Db      565 PYAQSIGRGTSPTLSEKIDTLTLAIGTYREHKSWEGLMRGRGDYSEWNAI 624
Qy      787 LYEDVLLKAKYOM 799
Db      625 QYEQV-----FTW 632

RESULT 12
US-09-606-304-10
; Sequence 10, Application US/09606304
; Patent No. 6483010
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; APPLICANT: Springer, Franziska
; APPLICANT: Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
```

CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/606,304  
FILING DATE: 28-Jun-2000  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/836,567  
FILING DATE: <Unknown>  
APPLICATION NUMBER: DE P 44 41 408.0  
FILING DATE: 10-NOV-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: AGREVO-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 641 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-606-304-10

Query Match 27.5%; Score 1176; DB 4; Length 641;  
Best Local Similarity 45.2%; Pred. No. 3.4e-99;  
Matches 250; Conservative 72; Mismatches 181; Indels 50; Gaps 12;

283 AVADAGSFEHQ--NHDSGLAGN-----VWVVVVAECSPMCKTGSLDVA 330  
94 SVAGDITVESHDIYANDRDLSEDTMEMETPIKLTNTITFTREAPSKTGLSDVC 153  
331 GALPKALAKGHRVWVVPY-----GDYEADVGVKRYXAGQDMEVNYFAYID 383  
154 GSLPVALARGRVWVVPYRLNGSPDEKXANVDLDVRAVHCFGDAGVAVHYEYRA 213  
384 GVDFFIDAPLFRH--ROEDTIG--SGRQEIEMRMILFCAAEVPMHVCQGVPGDG 438  
214 GVDWVVFVHSSICRDPYIGDIYAGFGNQ--FRFTLSHACEAPLVLTGFTTGE- 269  
439 NLVFIANDWHTALFVYLKAYYRDHGLMOTRSINVINIAHQGRGPVDEPFTLPEHY 498  
270 KCLFIANDWHTALVLLAAKRYPGYKARSIVAHINAHQVEPAVTTNNGLDPW 329  
499 LEHFLYDPV-----GGEHANYFAAGLCKADQVVVSPGYLMELKTVGGGGLDIT 550  
330 YGAVEMIFPTWARAHALDTGETVNLKGAIVADRIITVSGYSWEITTPPGSGLHLL 389  
551 RQNDWKTGRIYVNGIDNMENPEVDVHLKSDGYVTFSLGTLDSGRQCKEALQRELQVR 610  
390 SSRQSVNLNGITNGIDVNDMPSTDEHIAS---HXSINDL-SGVQCQCTDLQKELGPIR 444  
611 ADVPLGISTGRDGKGYEIIADAMPVVSODVQVLMGTRHDLSEMLRFEFHHDKV 670  
445 PDCPLIGTIGRIDYKGVIIISLAPELMONDVQVVMGSGEKKOYEDMRTETELFDKF 504  
671 RGVVFSVRLARITAGADALIMPSPFCGILNOLYAMAQTVPVVAVGSGVRTVPFD 730  
505 RAVGFNVFVSHRITAGCDILMPSPFCGILNOLYAMRGTITPIVHSTGSLRTVVDN 564

731 PNHSGL---GWTFDRBAKHLIALCHCIRTVDYESVRGLOERMSPQPSNEHAK 786  
565 PYAEGIGETGWTSPPLTSEKLDLTLLAIGTYEHSWEGIMRRGRMGHDSWENAAI 624

787 IYEDVTLKAKYOM 799  
625 QYEQV-----FTW 632

RESULT 13  
US-09-196-390-2  
Sequence 2, Application US/09.96390  
Patent No. 6307125

GENERAL INFORMATION:  
APPLICANT: Block, Martina  
APPLICANT: Lotz, Horst  
APPLICANT: Lutticke, Stephanie  
APPLICANT: Walter, Lemart  
APPLICANT: Froberg, Claus  
APPLICANT: Koestmann, Jens

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES  
FROM WHEAT WHICH ARE INVOLVED IN STARCH  
SYNTHESIS

TITLE OF INVENTION: SYNTHESIS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10020

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/196,390

CLASSIFICATION:  
FILING DATE:  
APPLICATION NUMBER: DE 196 21 588.9  
FILING DATE: 29-MAY-1996  
APPLICATION NUMBER: DE 196 36 917.7  
FILING DATE: 11-SEP-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP97/02793  
FILING DATE: 28-MAY-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Haley, Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: AGREVO-9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 671 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-196-390-2

Query Match 26.6%; Score 1138.5; DB 4; Length 671;  
Best Local Similarity 47.8%; Pred. No. 1e-95;  
Matches 237; Conservative 71; Mismatches 161; Indels 27; Gaps 9;

309 NVVVVVAECSPMCKTGSLDVGALPKALARGHRVWVVPY-----GDYEADVGVK 364  
55 SLVFTVGEAAPFAKSGGLDVGSLPLALARGHRVWVVPYRLNGSSDQKAYAKLYTAK 114  
365 YTK--AAGQDMEVNTFHAVIDGVVFIDAFVFRROEDTIG--SGRQEIEMRMILPCK 419

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Db      115 HIIPCGSGHEVTFEHEYRDNDVWVVDHPSY-HRPGSLYGNFGAFDNOFRYTLCCY 173
Qy      420 AAVEPMHVPDGGVPGDGNLVFIANDMHTALLPYLKAAYRDHGLMOYTRSIMVHNIA 479
Db      174 AACGAPILILEGGITYGQ-NCMFVNDMHASLVPVLAARXRYGYRDSRSTLVHNIA 232
Qy      480 HOGGKPVDERPFFTELEPHYL-----EHFRLYDPVGGEHANYPFAAGLKMDOVVVSP 531
Db      233 HOGVEPASTYFDLGLPEMYGALWVFPPEARHRLALDKGAANPLKGAVTADRLVTSQ 292
Qy      532 GYLVELTVEGGMGLHDIIRQNDWKTGRIYNGIDNMENPEVDVHLKSDGYTNFSLGTD 591
Db      293 GYSMEVTTABEGGOLNELLSSKSVLNGIYNGIDINDMNPTTKCLPH---HYSVDL- 347
Qy      592 SGKQCKEALQRELGLQVADVPVLLGFIQLDQKVEITADAMPVTSQDVLNLTG 651
Db      348 SGKAKCAELQKELGLPVRBDVPLIGFISLDYQKIDLIKMAIPELMREDVGFVNLGSG 407
Qy      652 RHDESMLRPEREHHDKVRGWSVRLAHRITAGADALLMPSREFEPCGLNOLYAMAYG 711
Db      408 DRIEGMKRSTESSYKDKFRGMVGSFVPSHRITAGCDILMPSREFEPCGLNOLYAMQY 467
Qy      712 TVPVVAHVGVDRDTPVPPDPF--NHSGLGTFDRAHKLIALGHCLTFYDYKESNR 768
Db      468 TVPVVHGIGLRDVTVEFNFPFGAKGEGTGWAFSPPLTVDXMLVLRTMSTFHEHKSWE 527
Qy      769 GLQERGMQDPSWEHA 784
Db      528 GLMKGMTKDTWDHA 543

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## RESULT 14

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US-08-941-445A-13
; Sequence 13, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanning
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 583 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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## US-08-941-445A-13

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Query Match      24.9%; Score 1066; DB 3; Length 583;
Best Local Similarity 41.5%; Pred. No. 3,7e-89;
Matches 248; Conservative 75; Mismatches 200; Indels 74; Gaps 14;

Qy      189 ATISIDKAPESVPAKPPSSGNSFVBSA;APRLDIDSDVEPELKKGAVIEAPNPX 248
Db      3 AELSRGAPRLPRLAPP-----LVPGHAPP-----AEPTEPA 40
Qy      249 ALSPAPADVOEDIMDFEKTIIGFEEPYEAK----DDGNAVADAGSFEHGHNSGFLAGE 305
Db      41 STPPVPDAGLDI-----GLPBGIAEGSIDNTVVAASE-----QSEIIVGK 84
Qy      306 N-----VNAVVAVAECSPMCKTGGLGDVNAALPKALAKGHEVMVVPY-----GD 353
Db      85 EQAPAKYQSIIVFTTGEASPYAKSGGLGDYQSLPALAARGHVVVVMPTYLNGTSDKN 144
Qy      354 YEEAYDVGRKRYKAAQDMENVNFHAYIDGVDVFTIDAPLFRROEDITYG--GSRQEI 410
Db      145 YANAFYTEKHRIIPCFGGEHEVTFEHEYRDSYDWWFVDHPSY-HRPGNLYGDKFGATGDN 203
Qy      411 MKRMTLPCKAAVEPMHVPDGGVPGDGNLVFIANDMHTALLPYLKAAYRDHGLMOYTR 470
Db      204 QPRTYLLCYAACAPLILEGGITYGQ-NCMFVNDMHASLVPVLAARXRYGYRDSR 262
Qy      471 SIMVHNIAHOGRGFVDEPFFTELEPHYL-----EHFRLYDPVGGEHANYPFAAGLKM 522
Db      263 SILVHNIAHOGVEPASTYFDLGLPEMYGALWVFPPEARHRLALDKGAANPLKGAVT 322
Qy      523 ADQVVVSGYLMEIKTVGEGMGLHDIIRQNDWKTGRIYNGIDNMENPEVDVHLKSDGY 582
Db      323 ADRIYVSKISMEVTTABEGGOLNELLSSKSVLNGIYNGIDINDMNPTTKCLPH--- 378
Qy      583 TNFSLGTLDSGKQCKEALQRELGLQVADVPVLLGFIQLDQKVEITADAMPVTSQD 642
Db      379 CHYSVDL-SGKAKCAELQKELGLPVRBDVPLIGFISLDYQKIDLIKMAIPELMRED 437
Qy      643 VOLNMLGCRHDLJESMLHFEREHHDKVRGWSVRLAHRITAGADALLMPSREFEPCGL 702
Db      438 VQVPMGSDPPELBMWSTESIFDKRGMVGSFVPSHRITAGCDILMPSREFEPCGL 497
Qy      703 NOLYMAVGTVPVVAHVGVDRDTPVPPDPFNS---GLGWTFDRAHKLIALGHCL 756
Db      498 NOLYMQYGTVPVVAHVGVDRDVTVEFNFPFGAKGEGTGWAFSPPLTVDXMLVLR 554

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## RESULT 15

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US-08-941-445A-21
; Sequence 21, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanning
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:

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OM protein - protein search, using sw model

Run on: February 20, 2004, 11:12:48 ; Search time 38 seconds  
(without alignments)

4402.538 Million cell updates/sec

Title: US-10-018-418-4

Perfect score: 4276

Sequence: 1 MSSAVASASFTALASAPG.....SNEHAKUYEDVLKAYQW 799

Scoring table: BLOSUM62

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/prodata/1/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/prodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

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9: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep:\*

10: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep:\*

11: /cgn2\_6/prodata/1/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep:\*

14: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6/prodata/1/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep:\*

17: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

18: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4075	95.3	799	10	US-09-952-677-6
2	2516.5	58.9	641	12	US-10-272-291-8
3	2163	50.6	801	12	US-10-044-543-26
4	2150.3	50.3	767	15	US-10-284-668-8
5	2069.5	48.4	477	12	US-10-272-291-7
6	2063	48.2	690	12	US-10-044-543-6
7	2059	48.2	658	15	US-10-284-668-10
8	1176	27.5	641	15	US-10-284-668-10
9	1138.5	26.6	459	15	US-09-952-677-2
10	1004.5	23.5	459	15	US-10-284-668-4
11	950	22.2	636	15	US-10-138-075-4
12	907	21.2	616	12	US-10-044-543-14
13	891.5	20.8	599	15	US-10-138-075-5
14	885	20.7	615	12	US-10-044-543-2
15	869	20.3	600	12	US-10-272-291-3

16	869	20.3	605	12	US-10-272-291-6	Sequence 6, Appli
17	869	20.3	606	12	US-10-228-063-8	Sequence 8, Appli
18	867	20.3	600	12	US-10-044-543-22	Sequence 22, Appli
19	865	20.2	609	15	US-10-138-075-2	Sequence 2, Appli
20	863	20.2	600	12	US-10-272-291-4	Sequence 2, Appli
21	841	19.7	634	12	US-10-044-543-18	Sequence 18, Appli
22	770	18.0	466	12	US-10-369-453-2879	Sequence 279, Ap
23	758	17.7	461	12	US-10-369-453-20916	Sequence 20916, A
24	718.5	16.8	483	12	US-10-369-453-4757	Sequence 4757, Ap
25	718.5	16.8	483	12	US-10-369-453-7516	Sequence 7516, Ap
26	717	16.8	484	12	US-10-369-453-18358	Sequence 18358, A
27	713.5	16.7	484	12	US-10-369-453-23266	Sequence 23266, A
28	712	16.7	476	12	US-10-369-453-1676	Sequence 1676, A
29	691.5	16.2	466	12	US-10-369-453-9895	Sequence 9895, Ap
30	686.5	16.1	465	12	US-10-369-453-19030	Sequence 19030, A
31	686	16.0	459	12	US-10-369-453-19180	Sequence 19180, A
32	681	15.9	476	12	US-10-369-453-17179	Sequence 17179, A
33	674	15.8	460	12	US-10-369-453-19894	Sequence 19894, A
34	644	15.1	473	12	US-10-369-453-9988	Sequence 9988, Ap
35	639	14.9	476	12	US-10-369-453-20431	Sequence 20431, A
36	633	14.8	477	12	US-10-369-453-2777	Sequence 2777, Ap
37	628	14.7	481	12	US-10-369-453-10573	Sequence 10573, A
38	625.5	14.6	479	12	US-10-369-453-19718	Sequence 19718, A
39	624.5	14.6	480	12	US-10-369-453-11375	Sequence 11375, A
40	624.5	14.6	480	12	US-10-369-453-14779	Sequence 14779, A
41	624.5	14.6	480	12	US-10-369-453-14933	Sequence 14933, A
42	624.5	14.6	480	12	US-10-369-453-15270	Sequence 15270, A
43	617.5	14.4	874	15	US-10-163-214-13	Sequence 13, Appli
44	604	14.1	477	12	US-10-369-453-23585	Sequence 23585, A
45	603	14.1	473	12	US-10-369-453-11532	Sequence 11532, A

## ALIGNMENTS

RESULT 1  
US-09-952-677-6  
Sequence 6, Appli  
Patent No. US20020138876A1  
GENERAL INFORMATION:

APPLICANT: Block, Martina

Loetz, Horst

Luticke, Stephanie

Walter, Lemnat

Froberg, Claus

Kossmann, Jens

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES  
FROM WHEAT WHICH ARE INVOLVED IN STARCH  
SYNTHESIS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/952,677

FILING DATE: 14-Sep-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/196,390

FILING DATE: 19-No. US20020138876A1-1998

APPLICATION NUMBER: DE 196 21 538.9

FILING DATE: 29-MAY-1996

APPLICATION NUMBER: DE 196 36 917.7

FILING DATE: 11-SEP-1996

APPLICATION NUMBER: PCT/EP97/02793



Mon Feb 23 11:51:13 2004

us-10-018-418-4.rapb

Page 2

FILING DATE: 28-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley, Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: AGREVO-9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 799 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-952-677-6

Query Match 95.3%; Score 4075; DB 10; Length 799;  
Best Local Similarity 95.6%; Pred. No. 2,2e-312;  
Matches 764; Conservative 7; Mismatches 28; Indels 0; Gaps 0;

QY 1 MSSAVASAFILASAPGRSRRARVSAAPPAGAGRLHMPMPDPORTARDGVAARA 60  
DB 1 MSSAVASAFILASAPGRSRRARVSAAPPAGAGRLHMPMPDPORTARDGVAARA 60  
QY 61 AGKDAEVDDDAASAROPRARRGAAITKVAERDPVYTLDRDAAGAPAPAPRODAAR 120  
DB 61 AGKDAEVDDDAASAROPRARRGAAITKVAERDPVYTLDRDAAGAPAPAPRODAAR 120  
QY 121 PPSNNGPVNGENKSTGGGATKDSGLPAPARAHPSTONRVVNGENKANYASPTSLA 180  
DB 121 PPSNNGPVNGENKSTGGGATKDSGLPAPARAHPSTONRVVNGENKANYASPTSLA 180  
QY 181 EVVAPDSAAITISIDKAPESVVPAAEKPPSSGSNFVVSASAPRLIDSDVEPELKKGAVI 240  
DB 181 EVVAPDSAAITISIDKAPESVVPAAEKPPSSGSNFVVSASAPRLIDSDVEPELKKGAVI 240  
QY 241 VEEAPNPKALSPAPAPVOEDLMPFKYIGFEEVEAKDGMVAVDADAGSEHONHDSG 300  
DB 241 VEEAPNPKALSPAPAPVOEDLMPFKYIGFEEVEAKDGMVAVDADAGSEHONHDSG 300  
QY 301 PLAGENWNVVVAASCSPMCKTGLGADVAGALPKALAKGHRVNVVPEYGDYEAYDV 360  
DB 301 PLAGENWNVVVAASCSPMCKTGLGADVAGALPKALAKGHRVNVVPEYGDYEAYDV 360  
QY 361 GVRKRYKAAQDMENVTFHAYIDGVDFIDAPFRROEDYIGSSQOEMKRMILFCKA 420  
DB 361 GVRKRYKAAQDMENVTFHAYIDGVDFIDAPFRROEDYIGSSQOEMKRMILFCKA 420  
QY 421 AVEVPWHPVCGGVPGDGNLVFIANDMHTALLPYLKAYYRDHGLMOYTSIMVTHIAH 480  
DB 421 AVEVPWHPVCGGVPGDGNLVFIANDMHTALLPYLKAYYRDHGLMOYTSIMVTHIAH 480  
QY 481 QGRGVDEFPPTLEPERYLEHRLYDPVYGEHANYFAAGLKNADQVYVVSFGYIMELKTV 540  
DB 481 QGRGVDEFPPTLEPERYLEHRLYDPVYGEHANYFAAGLKNADQVYVVSFGYIMELKTV 540  
QY 541 EGGWGLHDIIRONDKTRGIYNGIDNMENPEVDVHLKSDGYTNFSLGTLDSGRCKEA 600  
DB 541 EGGWGLHDIIRONDKTRGIYNGIDNMENPEVDVHLKSDGYTNFSLGTLDSGRCKEA 600  
QY 601 LQREIGLOVRADVPLIGFIRGLDGKGYEIIADAMPWVSODVOLVMLGTRHDLJESMLQ 660  
DB 601 LQREIGLOVRADVPLIGFIRGLDGKGYEIIADAMPWVSODVOLVMLGTRHDLJESMLQ 660  
QY 661 HEEHHDHVRGWSVYRLAHRTAGADALIMPSRFPCGILNOLYMAAYGVVAVAG 720  
DB 661 HEEHHDHVRGWSVYRLAHRTAGADALIMPSRFPCGILNOLYMAAYGVVAVAG 720  
QY 721 GVRDTPVPFDPNHSGLGWTDFRADAHKLIEALGHCLTTPDYKESWRGLQERMSODFS 780  
DB 721 GVRDTPVPFDPNHSGLGWTDFRADAHKLIEALGHCLTTPDYKESWRGLQERMSODFS 780

QY 781 WEHAAKLYEDVLLKAYQW 799  
DB 781 WEHAAKLYEDVLLKAYQW 799

RESULT 2  
US-10-272-291-8  
Sequence 8, Application US/10272291  
Publication No. US20030150023A1  
GENERAL INFORMATION:  
APPLICANT: Exseed Genetics  
TITLE OF INVENTION: Starch  
FILE REFERENCE:  
CURRENT FILING DATE: 2002-10-17  
PRIOR APPLICATION NUMBER: 60/329,525  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 641  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Starch Synthase Iia (SsIIa)  
US-10-272-291-8

Query Match 58.9%; Score 2516.5; DB 12; Length 641;  
Best Local Similarity 66.2%; Pred. No. 1,2e-189;  
Matches 493; Conservative 54; Mismatches 93; Indels 105; Gaps 8;

QY 56 VAAABAGKDKARVDDDAASAROPRARRGAAITKVAERDPVYTLDRDAAGAPAPAPR 115  
DB 1 VAAABAGKDKARVDDDAASAROPRARRGAAITKVAERDPVYTLDRDAAGAPAPAPR 115  
QY 116 QDAAPPSMNQTPVNGENKSTGGGATKDSGLPAPARAHPSTONRVVNGENKANYASP 175  
DB 116 QDAAPPSMNQTPVNGENKSTGGGATKDSGLPAPARAHPSTONRVVNGENKANYASP 175  
QY 176 PSTIAVVAAPSATISIDKAPESVVPAAEKPPSSGSNFVVSASAPRLIDSDVEPEL 235  
DB 176 PSTIAVVAAPSATISIDKAPESVVPAAEKPPSSGSNFVVSASAPRLIDSDVEPEL 235  
QY 236 KCAVIVEEAPNPKALSPAPAPVOEDLMPFKYIGFEEVEAKDGMVAVDADAGSEH 294  
DB 236 KCAVIVEEAPNPKALSPAPAPVOEDLMPFKYIGFEEVEAKDGMVAVDADAGSEH 294  
QY 295 QNHSQGPLAGENVNVVVAASCSPMCKTGLGADVAGALPKALAKGHRVNVVPEYGDY 354  
DB 295 QNHSQGPLAGENVNVVVAASCSPMCKTGLGADVAGALPKALAKGHRVNVVPEYGDY 354  
QY 355 EEAADVGRKRYKAAQDMENVTFHAYIDGVDFIDAPFRROEDYIGSSQOEMKRM 414  
DB 355 EEAADVGRKRYKAAQDMENVTFHAYIDGVDFIDAPFRROEDYIGSSQOEMKRM 414  
QY 415 IIFCKAAVEVPWHPVCGGVPGDGNLVFIANDMHTALLPYLKAYYRDHGLMOYTSIMV 474  
DB 415 IIFCKAAVEVPWHPVCGGVPGDGNLVFIANDMHTALLPYLKAYYRDHGLMOYTSIMV 474  
QY 475 IHNIAHQSGLVDEFPPTLEPERYLEHRLYDPVYGEHANYFAAGLKNADQVYVVSFGYL 534  
DB 475 IHNIAHQSGLVDEFPPTLEPERYLEHRLYDPVYGEHANYFAAGLKNADQVYVVSFGYL 534  
QY 535 WEIKTYEGSGWGLHDIIRONDKTRGIYNGIDNMENPEVDVHLKSDGYTNFSLGTLDSG 594  
DB 535 WEIKTYEGSGWGLHDIIRONDKTRGIYNGIDNMENPEVDVHLKSDGYTNFSLGTLDSG 594  
QY 595 ROCKEALORELGLQVRADVPLIGFIRGLDGKGYEIIADAMPWVSODVOLVMLGTRH 654  
DB 595 ROCKEALORELGLQVRADVPLIGFIRGLDGKGYEIIADAMPWVSODVOLVMLGTRH 654  
QY 655 LBSMLHFEREHDHVRGWSVYRLAHRTAGADALIMPSRFPCGILNOLYMAAYGVV 714  
DB 655 LBSMLHFEREHDHVRGWSVYRLAHRTAGADALIMPSRFPCGILNOLYMAAYGVV 714

Db 512 LERMLCHLEHREHNKRGVSVPMARHTAGADVLVMSRPEPCGLNQLYAMAVGTVP 571  
QY 715 VHAAGVBDTVPPEPFPNHSIGTFFDPAEAKHLEIGHCLRTYRDKESWRGLQERG 774  
Db 572 VVAIV-----AGLGWTFDPAEANKLIEALRHCLDITYRKXGESKSLQARG 616  
QY 775 MSODFSEMEHAKLYEDVLKAKYQW 799  
Db 617 MSODLSMDHAAELYEDVLKAKYQW 641

## RESULT 3

US-10-044-543-26  
; Sequence 26, Application US/10044543  
; Publication No. US20030135883A1  
; GENERAL INFORMATION:  
; APPLICANT: Singletary, George  
; APPLICANT: Zhou, Lan  
; TITLE OF INVENTION: No. US20030135883A1el Starch Synthase Polynucleotides  
; TITLE OF INVENTION: and Their Use in the Production of New Starches  
; FILE REFERENCE: 1144D  
; CURRENT APPLICATION NUMBER: US/10/044,543  
; CURRENT FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: 09/388,743  
; PRIOR FILING DATE: 1999-09-02  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 26  
; LENGTH: 801  
; TYPE: PRN  
; ORGANISM: Typha latifolia  
US-10-044-543-26

Query Match 50.6%; Score 2163; DB 12; Length 801;  
Best Local Similarity 60.7%; Pred. No. 1.2e-161;  
Matches 42; Conservative 8; Mismatches 151; Indels 41; Gaps 9;

QY 134 KSTGGGATKDSG--LPAPAPAPSTQNVPNVNGENKAVASPPPSIAEVAAPDSAAIT 191  
Db 21 RATGKSGSFEEGEBRGVAGVDDALRATTIDKSE--TLAHSNLLQOLAKRNIVS 78  
QY 192 SI--SDKAF-----SVPAEKPPSSG-----SNFVVA-- 219  
Db 79 SIRSDVKEKENDSSVYKENTLESSEGGNGKYSKSAVNNYSQLAQDDTSENPLVNSG 138  
QY 220 SAPRLDIDSVPEPLKGAIVIEEAPNPKALSP--AAPVQEDLDWFKYIGFEEPVDA 277  
Db 139 GSPKDNVEA--VEFVROSAVDAFGRPEPSIGTKLISPYLEAESGAEEAEDLVRA 197  
QY 278 KDDMAVADAAGSEFHONDSGLAGENVNVVVAACSPWCKTGSLGDAVAGALPKAL 337  
Db 198 KLSVAVKCDLNPGE--ENEVPLPLAGANNMIIVAAECAPSKSGGLDVGALPKAL 255  
QY 338 AKGGRVAVVPRVGYDEAYDVGRKRYKAAGDMEVNTFAVIDGVDFVFIADAPLRH 387  
Db 256 ARGHRVAVVPRVGYDEAYDVGRKRYKAAGDMEVNTFAVIDGVDFVFIADAPLRH 387  
QY 398 RQEDYGGSRQIMKRWILPCKAVEVPMVHPGCGVPGDGNVFIANDWHTALLPYLYK 457  
Db 316 RGNRIYBGRVDILKRMILPCKAAVEVPMVHPGCGVPGDGNVFIANDWHTALLPYLYK 375  
QY 458 AAYRDHGLMAYTRSIMYIHNIHQGRGVDEFPTELPEHYLEHFRLLYDPVGEHANYFA 517  
Db 376 AAYRDHGLMAYTRSIMYIHNIHQGRGVDEFPTELPEHYLEHFRLLYDPVGEHANYFA 517  
QY 518 AGLKADQVAVVSHGYVWELKTSBGWGLHDIIRQNMKRGVINGIDNNEMNPEVAVHL 577  
Db 436 AGLKADQVAVVSHGYVWELKTSBGWGLHDIIRQNMKRGVINGIDNNEMNPEVAVHL 577  
QY 578 KSDGYNFSGLTDSGKQCKEALQRELGLQVADVPVLGFTIGRLDQCKVEIITADMPV 637  
Db 496 KSDGYNFSGLTDSGKQCKEALQRELGLQVADVPVLGFTIGRLDQCKVEIITADMPV 637

QY 638 IVSODVOLVNLGTRHDLSEMLRFEHREHDEYRGWGESVRLAHRITAGADALLMPSRF 697  
Db 556 IVSHDVQVWNLGTRHDLSEMLRFEHREHDEYRGWGESVRLAHRITAGADALLMPSRF 615  
QY 698 EPCGLNQLYAMAVGTVVHAAGVBDTVPPEPFPNHSIGTFFDPAEAKHLEIGHCL 757  
Db 616 EPCGLNQLYAMAVGTVVHAAGVBDTVPPEPFPNHSIGTFFDPAEAKHLEIGHCL 757  
QY 758 RTYDKESWRGLQERGMSODFSEMEHAKLYEDVLKAKYQW 799  
Db 676 RTYDKESWRGLQERGMSODFSEMEHAKLYEDVLKAKYQW 717

## RESULT 4

US-10-284-668-8  
; Sequence 8, Application US/10284668  
; Publication No. US20030106100A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosemann, Jens  
; APPLICANT: Springer, Franziska  
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES  
; INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC  
; PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/284,668  
; FILING DATE: 29-Oct-2002  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/836,557  
; FILING DATE: 24-JUL-1997  
; APPLICATION NUMBER: PCT/EP95/04415  
; FILING DATE: 09-NOV-1995  
; APPLICATION NUMBER: DE P 44 41 408.0  
; FILING DATE: 10-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: Agrevo-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-596-9000  
; TELEFAX: 212-596-8090  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 767 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-10-284-668-8

Query Match 50.3%; Score 2150.5; DB 15; Length 767;  
Best Local Similarity 54.3%; Pred. No. 1.1e-160;  
Matches 42; Conservative 104; Mismatches 188; Indels 67; Gaps 10;

QY 34 HAGAGRLHPWPFPRTARDGVABARAGKXDARVDDAASAROPRARGGATVAERR 93  
Db 31 HSSREQMRIRKRVATGSEASADESNDIA--IQVTIKSKVLAQCDLLQIABRR 89  
QY 94 DEVKTLDRDA-----EGAPV-----PPAPRODAARPPSMNGTVPNGENKSTGGGGA 141

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Db      90 KVVSSISLANKGTIDGSGSLSDVIDPDVDKVVVVPSTAAPIPTVDKNT----- 144
Qy      142 TKOSGLPAPAPAPSTQNRVPVNGENKANA---SPPTSLAIVAPADEAATISIDKAP 198
Db      145 -----PPATISQDFVESREIKRDLADERAPPSRSSITA-SQGISIVSSKKT 191
Qy      199 ESVPAPKPPSSSGSNFVGSAPRLDID-----SDVEPELKGAIVIEEAPFKALSPPA 254
Db      192 LN-VPEPTPKSSQCTLLDVNSRKSIVDPGKTIQSYPSLRKSSASHVGEQRENLEGG 250
Qy      255 APAVOEDLWPKYITIGEEPEVEAKDGMVADNAGSFHHQNHDSQPLAGENNMYVVA 314
Db      251 AEANEET-----EDPVI-----DEKPPPLAGTNVNTILVA 282
Qy      315 AEGSPCKTGGLGPVAGALPKALAKRGHVVVVVYGYDEEAVDGVRCYTYAAGDME 374
Db      283 SECAPKCKTGGLGPVAGALPKALARHGRVNVVAPRDVPEPDGSKRTIYVDQDVE 342
Qy      375 VNYFHAVIDGVFVIDAPLFRHROEDITYGSSROELMKMTLCKAAVEVPMVPCGGVP 434
Db      343 VTYECAFIDGVDPFVIDSHMFRHIGNNIYGGNRVDILKRMVLFCKAIEVPMVPCGGVC 402
Qy      435 YGDNVLVFIANDMTALLPYLKAAYRDHGLMOYTRSMYIHNIAHQGRPVDEPPTTEL 494
Db      403 YGDNVLVFIANDMTALLPYLKAAYRDNGIMYTRSVLVIHNIAHQGRPLEDFSVDL 462
Qy      495 PEHYLEHRLYDPVGEHANYFAAGLKNADQVVVSPGYLMEKTYVEGGHGLDIIFOND 554
Db      463 PPHYVDPFKLYDPVGEHEFNIFAAGLKTADRVTVVSIGYSELTKTSGGGGLDQIINEND 522
Qy      555 WKTGIVVNCIDMNEPEVDVHLKSDGYTNFSLGTLDSGKQCKEALQRELGQVRAVP 614
Db      523 WKLQGVNIGIDTKENPELDVHLQSDGYTANYSLDTLQTKQCAALOKELIGLRYRDPV 582
Qy      615 LIGFIRGLDQKGVETIADAMPWIVSODVOLVMLGTGRHDLSEMLRHFEEHHDKYAV 674
Db      583 LIGFIRGLDPQKGVDLIAFASAMWQGVOLVMLGTGRDLQMLRQFECQNDKIRGV 642
Qy      675 GSVYTLARITAGADALIMPSRFPCCGINOLYAAVGTVPVHAVGVRDVPDPDENH 724
Db      643 GSVYTLSHRITAGADILMPSRFPCCGINOLYAAKGTITIPVHAVGIRDTVQDFDFNE 702
Qy      725 SGLGWTFPRAEAKLIEALGHCLRTYRDYKESWRLQGRGNSODFSWEHAAYEDVLLK 794
Db      703 SGLGWTFPRAEASQIHALGNCLTYREYKKSWEQICRCMTQDLSMDNAQNEEVILTA 762
Qy      795 AKYQW 799
Db      763 AKYQW 767

```

## RESULT 5

```

US-10-272-291-7
/ Sequence 7, Application US/102722291
/ Publication No. US20030150023A1
/ GENERAL INFORMATION:
/ APPLICANT: Exseed Genetics
/ TITLE OF INVENTION: Starch
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/272,291
/ CURRENT FILING DATE: 2002-10-17
/ PRIOR APPLICATION NUMBER: 60/329,525
/ PRIOR FILING DATE: 2001-10-01
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 7
/ LENGTH: 477
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE: Starch Synthase I1b-2 (N-terminally truncated
/ OTHER INFORMATION: SS11b)

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US-10-272-291-7
Query Match      48.4%; Score 2069.5; DB 12; Length 477;
Best Local Similarity 76.0%; Pred. No. 1,4e-154;
Matches 374; Conservative 47; Mismatches 56; Indels 15; Gaps 1;

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Qy      308 MNTVVVAECSPCKCTGGLGPVAGALPKALAGHRTMNVVVPYGVDEEAVDGVRCYK 367
Db      1 MNTVVVAECAPFKCTGGLGPVAGALPKALARHGRVNVVIPRYGEYAEKADLSVRRRYK 60
Qy      368 AAGDMEVNYFHAVIDGVFVIDAPLFRHROEDITYGSSROELMKMTLCKAAVEVPMH 427
Db      61 VAGDSEVTHYSITIDGVDPFVEAPRFRHANNIYGGERLDILKMTLFCKAAVEVPMY 120
Qy      428 VPCGVVPYGDNLVFIANDMTALLPYLKAAYRDHGLMOYTRSMYIHNIAHQGRPVD 487
Db      121 APCGGTVYGDNLVFIANDMTALLPYLKAAYRDNGIMYARSVLVIHNIAHQGRPVD 180
Qy      488 EPPFTELPEHYLEHRLYDPVGEHANYFAAGLKNADQVVVSPGYLMEKTYVEGGHGLH 547
Db      181 DPNVDLEHYTHDHFKLVDNIGDHSNVFAAGLKTADRVTVVSIGYSELTKTSGGGGLH 240
Qy      548 DIIRQNDKTRGIVNGIDNMEMPEVDVHLKSDGYTNFSLGTLDSGKQCKEALQRELG 607
Db      241 DIIRQNDKLGIVNGIDNMEMNPVAVDVLHSDYTYVTFETLDTGKRD----- 289
Qy      608 QVRADVPLIGFIRGLDQKGVETIADAMPWIVSODVOLVMLGTGRHDLSEMLRHFEEBH 667
Db      290 ----DVLIGFIRGLDHQKGVDTIADAIHWLAGDQVOLVMLGTGRADLEMLRFESEHS 345
Qy      668 DTVRGWVSPVLAHRTITAGADALIMPSRFPCCGINOLYAAVGTVPVHAVGVRDVP 727
Db      346 DKRAVWGSVPLARITAGADILMPSRFPCCGINOLYAAVGTVPVHAVGIRDTVA 405
Qy      728 PDPPNHSGLGWTFPRAEAKLIEALGHCLRTYRDYKESWRLQGRGNSODFSWEHAAY 787
Db      406 PDPPNDTGLGWTFPRAEAKWIDLSHCLTYRYKESWRACTARGAEDLSMDHAAYL 465
Qy      788 YEDVLLKAYQW 799
Db      466 YEDVLLKAYQW 477

```

## RESULT 6

```

US-10-044-543-6
/ Sequence 6, Application US/10044543
/ Publication No. US20030135883A1
/ GENERAL INFORMATION:
/ APPLICANT: Singletary, George
/ APPLICANT: Zhou, Ian
/ TITLE OF INVENTION: No. US20030135883A1el Starch Synthase Polynucleotides
/ TITLE OF INVENTION: and their use in the Production of New Starches
/ FILE REFERENCE: 1144D
/ CURRENT APPLICATION NUMBER: US/10/044,543
/ CURRENT FILING DATE: 2002-01-11
/ PRIOR APPLICATION NUMBER: 09/388,743
/ PRIOR FILING DATE: 1998-09-02
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 6
/ LENGTH: 690
/ TYPE: PRT
/ ORGANISM: Curcuma zedoaria
US-10-044-543-6

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```

Query Match      48.2%; Score 2063; DB 12; Length 690;
Best Local Similarity 56.0%; Pred. No. 7,8e-154;
Matches 404; Conservative 80; Mismatches 166; Indels 72; Gaps 9;
Qy      109 PAPAP-----PAPAP-----PSMNGTFVNGENKSTGGGATKDSGL-----PAP 150
Db      10 PAPPPGASCRLLHGGAPLGHSPICWAMNLCSTRFVAGLSEVKKGSXITLKHIDHTGS 69

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us-10-018-418-4.rapb

Page 5

QY 151 ARAA-----HSTQNRVFNENKANAASPTSTIAEVVAPDSATISIDKAPESVVP 203  
DB 70 AATRRFLNALYHCGQADLVPIHNRKSSGAVGRSNIND-IOEDSNODVDIADDSVAQOME 128  
QY 204 AEXPPSSGSNFVVSASAPRLDDSDVEPELKKG-----AVIVEAPNPKALSPAPAA 257  
DB 129 QSKVLEMOXRLLOQIIEK-NFSEETESYKXDEMLGIAEYMQTSNNOGAAP- 183  
QY 258 VOEDLMDPKKYIGFEEVEAKDGMVAVDAGSFEHHQNDSCPLAGENNVVVAAC 317  
DB 184 -----EEG-----NINSPLAGPNMNIILVAAC 208  
QY 318 SPWCKTGLGVAGALPKALAKGRHVMVVPVGYDVEEAYDVGKYYAAGOMEVNY 377  
DB 209 APWKTGGLGVAGALPKALAKGRHVMVVSFRIGNTPEPKETGNLKYVDQDMEIKY 268  
QY 378 FHAYIDGVDFIDAPLFRHROEDYIGSSROEIMKEMILFCCKAVEVPMHVPCCGVYGD 437  
DB 269 YHTYIDSVDFEIDSPIFRHIINDIYGNRVDLIKRMVLFCKAVEVPMHVPCCGVYGD 328  
QY 438 GNLVFIANDMTALLPYTLKAYYDHGLMOYTRSIMVHNIAQGRPVDEFFTLPEH 497  
DB 329 GNLVFIANDMTALLPYTLKACFRDGLMTYARCLVHNIAHQGRPLDPSYVDLPHD 388  
QY 498 YLHFRLYDPVGSBHANYFAAGLTMADQVVVSPGYLMEIKTVGGWGLHDIIRONDWKT 557  
DB 389 HIDEFRLLDDPVGSHFNIFAGIRADRVVTVSHGVAMELKTSCEGWLHEIINECHWK 448  
QY 558 RGIYNGIDNENNEVDVHLKSDGYTNPSTGLDSSGRCKEALQRLGIQVADVPILG 617  
DB 449 HGIYNGIDTHSMNKRFAHINSDGYTNPSTGLDSSGRCKEALQRLGIQVADVPILG 508  
QY 618 FIGLDGQKVEIITADAMPVIVSODVOLVMTGRHDLSEMLRFESEHHDIKYRWGFS 677  
DB 509 FIGLDHDKGIDILAEAMHVLVODLQIMLGTORPLEDLRFRERHNGKVRGWGFS 568  
QY 678 VRLAHRITAGADALLMPERFPCGLNOLYAMAYGTVPVHAAGVTRTTPPDPFNHSL 737  
DB 569 VRLAHRITAGADALLMPERFPCGLNOLYAMAYGTVPVHAAGVTRTTPPDPFNHSL 628  
QY 738 GATDRAAHKLIEALGHCLRTYDYKESNRGLQERGSODFSNEHAKLYEDVTLKXY 797  
DB 629 GATDRAAHKLIEALGHCLRTYDYKESNRGLQERGSODFSNEHAKLYEDVTLKXY 668  
QY 798 QW 799  
DB 689 QW 690

RESULT 7  
US-10-284-668-6  
; Sequence 6, Application US/10284668  
; Publication No. US20030106100A1  
GENERAL INFORMATION:  
APPLICANT: Kosmann, Jens  
; Springer, Franziska  
; Abel, Gernot  
TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES  
INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC  
PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/284,668  
FILING DATE: 29-Oct-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,567  
FILING DATE: 24-JUL-1997  
APPLICATION NUMBER: PCT/EP95/04415  
FILING DATE: 09-NOV-1995  
APPLICATION NUMBER: DE P 44 41 408.0  
FILING DATE: 10-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: Agrevo-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 558 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-284-668-6  
Query Match  
Best Local Similarity 73.7%; Pred. No. 1,2e-153;  
Matches 368; Conservative 62; Mismatches 69; Indels 0; Gaps 0;  
48.2%; Score 2059; DB 15; Length 558;  
QY 301 PLAGENNVNVVVAACEGSPWCKTGLGVAGALPKALAKGRHVMVVPVRYDVEEAYDV 360  
DB 60 PLAGENNVNVVVAACEGSPWCKTGLGVAGALPKALAKGRHVMVVPVRYDVEEAYDV 119  
QY 361 GVRKYKKAAGOMENYHAYIDGVDFEIDAPLFRHROEDYIGSSROEIMKEMILFCCKA 420  
DB 120 GVRKYKKAAGOMENYHAYIDGVDFEIDAPLFRHROEDYIGSSROEIMKEMILFCCKA 179  
QY 421 AVEVPMHVPCCGVYGDGNTLVFIANDMTALLPYTLKAYYDHGLMOYTRSIMVHNIAH 480  
DB 180 AVEVPMHVPCCGVYGDGNTLVFIANDMTALLPYTLKAYYDHGLMOYTRSIMVHNIAH 239  
QY 481 QGRGPVDEPPFTELBEHLEHFRLYDPVGSBHANYFAAGLTMADQVVVSPGYLMEIKTV 540  
DB 240 QGRGPVDEPPFTELBEHLEHFRLYDPVGSBHANYFAAGLTMADQVVVSPGYLMEIKTV 299  
QY 541 EGWGLHDIIRONDWKTGRIYVNGIDNENNEVDVHLKSDGYTNPSTGLDSSGRCKEAA 600  
DB 300 EGWGLHDIIRONDWKTGRIYVNGIDNENNEVDVHLKSDGYTNPSTGLDSSGRCKEAA 359  
QY 601 LQRELGLQVRAVPLPLGFIGRLDGQKVEIITADAMPVIVSODVOLVMTGRHDLSEMLR 660  
DB 360 LQRELGLQVRAVPLPLGFIGRLDGQKVEIITADAMPVIVSODVOLVMTGRHDLSEMLR 419  
QY 661 HFEREHDKYRWGFSYVLAHRITAGADALLMPERFPCGLNOLYAMAYGTVPVHAAGV 720  
DB 420 HFEREHDKYRWGFSYVLAHRITAGADALLMPERFPCGLNOLYAMAYGTVPVHAAGV 479  
QY 721 GVADYVPPDPFNHSLGWTFRABAHLKIEALGHCLRTYDYKESNRGLQERGSODFS 780  
DB 480 GVADYVPPDPFNHSLGWTFRABAHLKIEALGHCLRTYDYKESNRGLQERGSODFS 539  
QY 781 WEHAKLYEDVTLKAYYQW 799  
DB 540 WEHAKLYEDVTLKAYYQW 558

RESULT 8  
US-10-284-668-10  
; Sequence 10, Application US/10284668  
; Publication No. US20030106100A1  
GENERAL INFORMATION:

```

APPLICANT: Kossmann, Jens
           Springer, Franziska
           Abel, Gernot
TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
                    INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
                    PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/284,668
FILING DATE: 29-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,567
FILING DATE: 24-JUL-1997
APPLICATION NUMBER: PCT/EP95/04415
FILING DATE: 09-NOV-1995
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Aigrevo-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 641 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-284-668-10
Query Match      27.5%; Score 1176; DB 15; Length 641;
Best Local Similarity 45.2%; Pred. No. 6,1e-84;
Matches 250; Conservative 72; Mismatches 181; Indels 50; Gaps 12;
QY      283  AVADAGSEFHHQ--NHDSGLPAGN-----VNWVVVVAECSPMCKTGGI.GDVA 330
DB      94  SVAGATVYESHDIYANDRDLSDETEMEETPICTLNNIIFVTAAPARYKKTGLGIVC 153
QY      331  GALTALAKRGHRVNVVPRY-----GDYEAYDVGVKRYKRYAKAGDMEVNTYHATID 383
DB      154  GSLPVALARGRVNVVSPRYLNGSPDSEKXANAVDLVRATVHCFGDAEVAFAHEHYRA 213
QY      384  GVDPEFIAPLPRH---ROEDLYG--GSRQEIIMKMI.LFCKAAVEVPMHVPDGGVPYDGG 438
DB      214  GVDWVFVHSSYCRGTPYGDLYGAFGDNQ---FFTLISHAACAPLPLVPLDGSTTGE- 269
QY      439  NIVFIANDWHTALLLVYLKAYTRDHGLMOYTRSLVITININAHQSGRPVDEFFETLPRHY 498
DB      270  KCLFIANDWHTALLVPLLLAAKTRPYGVYKXARSIVAHNINIAHQVGPATYNNIGL.PQW 329
QY      499  LEHFIPLYPV-----GGEHANYFAAGLKKADQVVVSPGYLWELKTVSGMGIDHDI 550
DB      330  YGAVEMIFPTWARAHALDTGETVNYLKGAIYAVADILITVSGYSWEITTPREGYGLHELL 389
QY      551  RQNDWKTRGIVNGIDNMENPEVDVHLKSDGYTFNSLGLTDSGRQCKEALOREIGLOVR. 610
DB      390  SSRQAVLNGITNGIDVNDWNPSTDEIAA---HYSINDL-SGVQCKTDLQKELGLPR 444

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QY 611 ADVPLILGFGRLDGGKGVETIADAMPMTVOSQVQVLVNLGTGRHDLSEMLHPFREHHDKV 674  
 Db 445 PDDLILGFGRDLDYKAGVDILLSAIPBLMOMDVVYVNLGSGEKYEEMWHTENLPDCK 564  
 QY 671 RGNVGSVYLAARITAGADALLMPREFPCGYNOLYAMVGVTVVHAVAGVDTYPPFD 730  
 Db 505 RAVGGENVSVSHRIITAGCDILMPSRFPCGANOLYAMRYGTIPIVISTGRLRYVDEN 564  
 QY 731 PFNHSL-----GWTDRRAEAKHKLIEALGHCLRTYRDYKESVRGQERGSODFSFEHAK 786  
 Db 565 FPAQSGISGTCMTSPITSEKLDLTCLKAIGITTEKSSWEGLMRGMRGRDYSENAAL 624  
 QY 787 LYEDVLLKAKYOM 799  
 Db 625 QYEQV-----FTW 632

RESULT 9  
 US-09-952-677-2  
 Sequence 2, Application US/09952677  
 Patent No. US20020138876A1  
 GENERAL INFORMATION:  
 APPLICANT: Block, Martina  
 Lortz, Horst  
 Luticke, Stephanie  
 Walter, Lemart  
 Froberg, Claus  
 Koessmann, Jens  
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES  
 FROM WHEAT WHICH ARE INVOLVED IN STARCH  
 SYNTHESIS

NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 10020

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/952,677  
 FILING DATE: 14-Sep-2001

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/196,390  
 FILING DATE: 19-NO. US0020138876A1-1998  
 APPLICATION NUMBER: DE 196 21 588.9  
 FILING DATE: 29-MAY-1996  
 APPLICATION NUMBER: DE 196 36 917.7  
 FILING DATE: 11-SEP-1996  
 APPLICATION NUMBER: PCT/EP97/02793  
 FILING DATE: 28-MAY-1997

ATTORNEY/AGENT INFORMATION:  
 NAME: Haley, Jr., James F.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: AGREVC-9  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 596-9000  
 TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 671 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-952-677-2

Query Match 26.6%; Score 1138.5; DB 10; Length 671;  
 Best Local Similarity 47.8%; Pred. No. 5.9e-61;  
 Matches 237; Conservative 71; Mismatches 161; Indels 27; Gaps 9;

309 NVVVVAECSPMCKTGSLGVAGALPKALAKGRVWVVRVY---GDVEEYDVGVK 364  
 55 SIIVTGEAAPYAKSGSLGVCSLPALALAKGRVWVVRVYKLNSSDKYAKLYTK 114  
 365 YRK--AAGQMEVYFAYIDGVDFVFDAPLFRHGOEDYQ--GSRQEIEMKMLFCK 419  
 115 HIKIPCGSGHEVTFEFREYRDNDVWVDFHPSY-HRPGSLYGNFGAFGDNFRYLLCY 173  
 420 AAVEVPHVPCGVPGVDDGNLVFIANDMTALLPYLKAYRDHGMQYRSIMVHNIA 479  
 174 AACAPLILBDGYTIGQ-NCMFVNDMHASLVPLAAKTRPYGVYRDSRTLVHNA 232  
 480 HOGGVPDEPPELTPEHYL-----EHFRLYDPVGEHANYFAAGLMAQDVVVS 531  
 233 HQGVEPASTYPDGLPEEWYGALEWVPEWARHALLDKGAVNPLKAVVTADRIYVQ 292  
 532 GYLMLKTVBGGWGLHITRONDKTRGIYNGIDNMEWNEVVLKSDGYTFSLGTD 591  
 293 GYSNEVTTAAGGQGLNELSSRSVINGIDINDMNPITDKLPH---HYSVDL- 347  
 592 SGKQCKEALQRELGVARADVPPLGFIKRLDGQVEIADAMPWIVSGVOLVNLG 651  
 348 SGKAKCAELQKELGLVREDEVPLIGTIGLDYKGLDILKALPELMREDVQFVLGSG 407  
 652 RHLESMLRFRERHNDKVRGWVGSVLAHRTAGADALLMPSPFPCGLNLYMANG 711  
 408 DPEFGMWSTESSYKCKFRGWGFSVPVSHRTAGCDIILMPSRPPCGLNLYMANG 467  
 712 TVPVVAHVGVRDVPPEDPF---NHSGLGTFDRAEAKHLEALGCLRTYDYESNR 768  
 468 TVPVVHGTGLKLDVETFPNPGAKGEGTGMAFPLTVDKMLAKRTMSTFRHPSNE 527  
 769 GLQGRGMSQDFSWEHA 784  
 528 GLMRGKMTKDHWDHA 543

# RESULT 10

US-10-284-668-4  
 ; Sequence 4, Application US/10284668  
 ; Publication No. US20030106100A1  
 ; GENERAL INFORMATION:

APPLICANT: Kosmann, Jens  
 ; Springer, Franziska  
 ; Abel, Gernot

TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES  
 INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC

PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES

NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & NEAVE  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York

COUNTRY: USA  
 ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
 OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/284,668  
 FILING DATE: 29-Oct-2002

CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/836,567  
 FILING DATE: 24-Jul-1997

APPLICATION NUMBER: PCT/EP95/04415

FILING DATE: 09-NOV-1995  
 APPLICATION NUMBER: DE P 44 41 408.0  
 FILING DATE: 10-NOV-1994

## ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: Agrevo-4

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-596-9000  
 TELEFAX: 212-596-9090

## INFORMATION FOR SEQ ID NO: 4:

### SEQUENCE CHARACTERISTICS:

LENGTH: 459 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Query Match 23.5%; Score 1004.5; DB 15; Length 459;  
 Best Local Similarity 45.6%; Pred. No. 1.3e-70;  
 Matches 210; Conservative 63; Mismatches 157; Indels 31; Gaps 9;

357 AYDVGVRRKYRAAGQMEVYFAYIDGVDFVFDAPLFRH--ROEDYQ--GSRQEI 411  
 5 AYDLIVRAIVHCFGDAQVAFYHEFRAGVDWVFVDHSSYRPRPYGDIYGAFGDNQ--- 61  
 412 KRMILFCKAAVEVPHVPCGVPGDGNLVFIANDMTALLPYLKAYRDHGMQYTRS 471  
 62 FRFTLSHACAPLVLPFGFTYGE-KCLFLANDCNALVPLAAKTRPYGVYKQARS 120  
 472 IMVINIAHQRGVPDEPPELTPEHYLHFRLYDPV-----GGEHANYFAAGLMA 523  
 121 IVAHINIAHQVAPVATYNNILGLPPQYGAWEIFTWARAHALDTGTVAVLVKGA-LAVA 180  
 524 DOVVVVSQGYLMELKTGSGGGLHDIIRONDKTRGIYNGIDNMEWNEVVLKSDGYT 583  
 181 DRILTVSGYSWEITTFEGSGYGLHELLSSRSVINGIDINDMNPSTDEHAS----- 236  
 584 NFSLGTD-SGKQCKEALQRELGVARADVPPLGFIKRLDGQVEIADAMPWIVSQD 642  
 237 HYSINDLSPGKQCKTDQKELGLPIRPDCPLIGTIGLDYKGLDILKALPELMQND 296  
 643 VOLVNLGTRHDLSEMLRFRERHNDKVRGWVGSVLAHRTAGADALLMPSPFPCGL 702  
 297 VQVWVLGSGEKQYEDMWMHTENLFFDKFRAVGVNVPVSHRTAGCDIILMPSRPPCGL 356  
 703 NQLYMAVGVTVVAVAGVGRDVPPEDPF---NHSGLGTFDRAEAKHLEALGCLRT 758  
 357 NQLYMARVGTIPDIVHSTGLADTVDFNPVQDEKGETGTWTFSLSEKLFDTLKALIR 416  
 759 TYRDYESVRGIQERGMSQDFSWEHAALYEDVLKAYQW 799  
 417 TYTEHKSWEGLMRGMRDYSWENAAIYQVQV-----FTW 452

# RESULT 11

US-10-138-075-4  
 ; Sequence 4, Application US/10138075  
 ; Publication No. US2003008769A1  
 ; GENERAL INFORMATION:

APPLICANT: Broglio, Karen E.  
 ; Applicant: Butler, Karen H.

APPLICANT: Butler, Leslie T.  
 ; Applicant: Harvey, Jonathan E.

APPLICANT: Lightnet, Jonathan E.  
 ; Applicant: Orozco, Emil M.

TITLE OF INVENTION: Granule-Bound Starch Synthase  
 FILE REFERENCE: BB1474 NA

CURRENT APPLICATION NUMBER: US/10/138,075  
 CURRENT FILING DATE: 2002-05-02

PRIOR APPLICATION NUMBER: 60/288,315  
 PRIOR FILING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 5

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Page 8

SOFTWARE: Microsoft Office 97  
; SEQ ID NO 4  
; LENGTH: 636  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-138-075-4

Query Match 22.8%; Score 950; DB 15; Length 636;  
Best Local Similarity 40.6%; Pred. No. 4e-66;  
Matches 216; Conservative 76; Mismatches 166; Indels 74; Gaps 12;

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QY 308 MNVVVVAAGSPMCKTGGLGADVAGALPKALAKGHRMMVVPYRGDYEAADVGYKRYK 367
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 106 MTFIIIGTEVAFPKCKTGGLGADVAGLPPALAGFGRMTIVPRYDQKAMDTSVIVLK 165
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 368 AAGDMENVYFHAVIDGVDFVFDAPLFRHROEDYGGSRQEI-----MKRMI 415
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 166 VGDTEKVRFFHCYKRGVDVRFVDHPWF---LEKVMGKTGKLYGPTGNDYEDNQLRFS 222
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 416 LFGCAAVEVPMHVPCCGV-----PYGDNLVFIANDMHTALLPYLKAAYYRDGLMQYTR 470
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 223 LFCQALAEAPRLVLNLSKSYSGPYGE-DVIFVANDMHTALLPCYLKSMYQSHGITYNNR 281
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 471 SIMVHNIAHQGRPVDEFPFTELEPHYLEHFLYD---PVGGEHANYFAAGIKMADQV 526
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 282 VVFCIHNIAYGGRPAFADFSLNLPDQFKSFPDIDGHVKKPVVGRKINMKAGILIESWV 341
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 527 VVVSFGYLMELKTEG---GWSGLHDIIRQ---NDMKTRGIVNGIDNMEWNEVDVHLKSDG 581
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 342 ITVSPNTAKEL--VSGPDKGVELNIIKIDDDGLVINGMDVQNMETTDKTYLA--- 396
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 582 YTNESLGLDSGKQCKEALQRELQVRAVPLLGFTGLDGQGYEIIADAMPWIVSQ 641
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 397 -VKVDVSTVLBAKLLKALQAEVGLPYDRNIPILIGFGRLEBCKSGSDILAEMIPCKIK 455
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 642 DVQVLMGTGRHDESMLRHFEREHNDKVRGWFVSRLAHRITAGADALLMPSRFPCCG 701
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 456 NVQIVAGTGRKKQKQLEELIEISTPDARGVAKENPLAMITAGADFLVSRFEPCCG 515
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 702 LNOYAMAAGTVPVHNAVGVADTV-----PPDPFNHSGLGWTFEDRAE 745
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 516 LIQQAQWYGVPIYASTGGLVDIVYKSGFTGFGMGAENVECDAPVADVAISKTVKRAL 575
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 746 A---HKITEALGHLRTYRDYKESWRGLQERGSQDSWHAAKYEDVLL 793
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 576 AVYGPATFETELIKNC-----MAQDLSMKGPAKMEVEVLL 609
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 12

US-10-044-543-14  
; Sequence 14; Application US/10044543  
; Publication No. US2003013583A1  
; GENERAL INFORMATION:  
; APPLICANT: Singletary, George  
; APPLICANT: Zhou, Ian  
; TITLE OF INVENTION: and their use in the Production of New Starches  
; FILE REFERENCE: 1144D  
; CURRENT APPLICATION NUMBER: US/10/044,543  
; CURRENT FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: 09/388,743  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 616  
; TYPE: PRT  
; ORGANISM: Canina edulis  
US-10-044-543-14

Query Match 21.2%; Score 907; DB 12; Length 616;  
Best Local Similarity 41.8%; Pred. No. 9.3e-63;  
Matches 216; Conservative 71; Mismatches 182; Indels 48; Gaps 14;

```
QY 308 MNVVVVAAGSPMCKTGGLGADVAGALPKALAKGHRMMVVPYRGDYEAADVGYKRYK 367
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 90 MNLVFGCEVAPMSKTTGLGADVAGLRLPAPYALIGHRMVTVPRYDQKMDTSVIVLEK 149
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 368 AAGDMENVYFHAVIDGVDFVFDAPLFRHROEDYGGSRQEI-----MKRMI 415
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 150 VGDTEKVRFFHCYKRGVDVRFVDHPWF---LEKVMGKTGKLYGPTGNDYEDNQLRFS 206
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 416 LFGCAAVEVPMHVPCCGV-----PYGDNLVFIANDMHTALLPYLKAAYYRDGLMQYTR 470
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 207 LFCQALAEAPRLVLNLSKSYSGPYGD-DVIFVANDMHTALLPCYLKSMYQSHGITYNNR 265
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 471 SIMVHNIAHQGRPVDEFPFTELEPHYLEHFLYD---PVGGEHANYFAAGIKMADQV 526
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 266 VAFCHNIAYGGRPAFADFSLNLPDQFKSFPDIDGHVKKPVVGRKINMKAGIIECDRC 325
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 527 VVVSFGYLMELKTEG---GWSGLHDIIRQ---NDMKTRGIVNGIDNMEWNEVDVHLKSDG 584
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 326 LTVSEFYAQELVSGVEKVELGNILRM---KTIQGINMDITBMBPLTDKTYLS---TN 378
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 585 FSLGLDSGKQCKEALQRELQVRAVPLLGFTGLDGQGYEIIADAMPWIVSQ 644
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 379 YDATTVDLAKLCKEALQAEVGLPYDRNIPILIGFGRLEBCKSGSDILAEMIPCKIK 438
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 645 LVMLGTGRHDESMLRHFEREHNDKVRGWFVSRLAHRITAGADALLMPSRFPCCG 704
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 439 VIVLTGTRKKQKLESELTLLEEMFPDKFRAHLKFNPLAHAIAGADFLVSRFEPCCG 498
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 705 LYAMAAGTVPVHNAVGVADTVPP-FDPFNHSGLGWTF-----DRAAKLIEALGHC 756
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 499 LQAMRYGTLPMCKSTGGLVDIVYKSGFTGFGMGAENVECDAPVADVAISKTVKRA 554
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 757 LRTYRDYKESWRGLQERMSQDSWHAAKYEDVLL 793
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 555 LKRYG--TPAFVEMIKCNODLSWKGPAKMEVEVLL 589
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 13

US-10-138-075-5  
; Sequence 5; Application US/10138075  
; Publication No. US2003008769A1  
; GENERAL INFORMATION:  
; APPLICANT: Broglio, Karen E.  
; APPLICANT: Butler, Karlene H.  
; APPLICANT: Harwell, Leslie T.  
; APPLICANT: Lightner, Jonathan E.  
; APPLICANT: Orozco, Emil M.  
; TITLE OF INVENTION: Granule-Bound Starch Synthase  
; FILE REFERENCE: B01474 NA  
; CURRENT APPLICATION NUMBER: US/10/138,075  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: 60/288,315  
; PRIOR FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 5  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
US-10-138-075-5

Query Match 20.8%; Score 891.5; DB 15; Length 599;  
Best Local Similarity 37.4%; Pred. No. 1.5e-61;  
Matches 199; Conservative 93; Mismatches 205; Indels 35; Gaps 12;

```
QY 288 AGSFHHON--HDSGLAGENVVVAAGSPMCKTGGLGADVAGALPKALAKGHRVM 345
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 50 ATNYGTHRSSRPAIVISTGMPILIFATVHPMCKTGGLGADVAGLPPALAMGHRVM 109
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 346 VVPRYGDYEAADVGVKRYKAAAGDMENVYFHAVIDGVDFVFDAPLFRHROEDYV- 404
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 110 TIAPRYDQKMDTMDTVLVEVIVGRTETVRFFHCYKRGVDVRFVDHPWF---LEKVMGK 166
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```



QY 405 -GSR-----OETMKRILFCRAAVEPWHVPCGV----PYGDNLVFIANDWH 448  
 DB 167 TGSXLYPTGTDTDRDQLEFCLLCALAEPRVLTNNSEYSGPYGE-NVVFVANDWH 225  
 QY 449 TALPPLYKAYRDHLMQYTRSIMVHNTAHQGRGVDEFPFTELEHLEHRLVD-- 506  
 DB 226 TAVIPCLIKMYKONGIYNAKAFCHINTAYQGRFPRVDPPELLNPESEMPSEDFDGH 285  
 QY 507 --PVGSHANYFAAGLRKADQVVVSPGYIMELKT-VEGWSGLHDIIRQNDMKTREGIVG 563  
 DB 286 VKPVGKRIKMMKAGITECDVVLVSPHYVELTSGPEKGEVLGVRAPLEFT-GIVNG 344  
 QY 564 IDNMENPDEVVHLKSDGYTNFSLGTLDSGRCKEKLQRELGQVADVPILGTLGLD 623  
 DB 345 MDVVDKMPNDKTYIS---VKYNTTVAEAPALNKEITLQAEVGLPVDSSIPVIVFGLRLE 400  
 QY 624 GQKGVETIADAMPWIVSQDVQVLMGTRHDLSMLHFEREHNDKYRGWVGESVRLAHR 683  
 DB 401 EQKSDILIAIPFELBENVOIIVLGNGKKKEEELMLEAKYQONARGLAKFVPLAHM 460  
 QY 684 ITAGADALIMSPREPCGLNOLYMAAYGTVPVYNAVGVADTPRP-FDPFNHSLGTLTPD 742  
 DB 461 MFAGANFTIVSRREPCGLIQLQGRYGVTPICSTGGLVDTVEGVTGFHMGSENVFE 520  
 QY 743 RAEAKLIEALGHCLRTYRDYK-ESWRLQERGMSCDPSFWEHALEYDVL 793  
 DB 521 TVDPADVAAVASNTVRALKQYKTSFHAMVQNCMAQDLSSWKPAAKMEBAL 572

## RESULT 14

US-10-044-543-2  
 ; Sequence 2, Application US/10044543  
 ; Publication No. US20030135883A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Singletary, George  
 ; APPLICANT: Zhou, Ian  
 ; TITLE OF INVENTION: No. US20030135883A1 Starch Synthase Polynucleotides  
 ; TITLE OF INVENTION: and their use in the production of New Starches  
 ; FILE REFERENCE: 1144D  
 ; CURRENT APPLICATION NUMBER: US/10/044,543  
 ; CURRENT FILING DATE: 2002-01-11  
 ; PRIOR APPLICATION NUMBER: 09/386,743  
 ; PRIOR FILING DATE: 1999-09-02  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 615  
 ; TYPE: PRT  
 ; ORGANISM: Curcuma zedoaria  
 ; US-10-044-543-2

Query Match 20.7%; Score 885; DB 12; Length 615;  
 Best Local Similarity 40.2%; Pred. No. 5e-61;  
 Matches 206; Conservative 78; Mismatches 190; Indels 38; Gaps 11;

QY 308 MNVVVVAACSPMCKTGGIGDVGALPKALAKRGHRVWVVRVYGDYEADVGRKYYK 367  
 DB 89 MMLTVAAEAVAPMSKTGGIGDVGGLPPMAKAGKRVTTIAPRHQYKQDMDTAVVELK 148  
 QY 368 AAGQDEWVYFAYIDGVFVIDAPLFRHQEDITYG-----SRQEMIKRMILFC 418  
 DB 149 VQDRLETRAFHFCYKRGVDRVFDHPLFLKVMGKTKIYGPVTRTDYEDNQRFCLC 208  
 QY 419 KAAVEPWHVPCGVPGD---GNVFTANDMHTALLPVYLKA-YYRHHGLMQYTRSLMV 474  
 DB 209 LATELTFRVLPNNNNKTSRKGEDLFTANDMHTALLPCYLTIVYQAHGGLYKAAKVAFC 268  
 QY 475 IHNIAHQGRPVDEFPFTELEHLEHRLVD---PVGSHANYFAAGLRKADQVVVVS 530  
 DB 269 IHNIAHQGRFAFEDFSRLNLPDFTKSSFDFTDGYAKPIKRIKMMKAGLIESRPLTVS 328  
 QY 531 PGYIMELKT-VEGWSGLHDIIRQNDMKT-REGIVNDIMMENPDEVVHLKSDGYTNFSLG 588

DB 329 PYYAOELVSGIDKVELNNTLR--LKITCGILNMDTNNMNPSTDKITYA---NYDAT 381  
 QY 589 TLDSGRCKEKLQRELGQVADVPILGTLGRDQKGVETIADAMPWIVSQDVQVLM 648  
 DB 382 TWAEKAPLNKEALQAEVGLPVNSKIPVIAFTIGRLEEGKSDILIAEAIKPFDPDOVQIVL 441  
 QY 649 GTRHDLSMLHFEREHNDKYRGWVGESVRLARITAGADALIMSPREPCGLNOLYAM 708  
 DB 442 GTGKKLREQLALDEFPDPRAMKKNIPLAGIMAGAILVPSRFBPGGLIQLQGM 501  
 QY 709 AYGTVPVNAVGVADTPRPDPFNHSLGTLTF-----DRAEAKLIEALGHCLRTYR 761  
 DB 502 RYGTSMCTTGGLVDTVEGVTGFHMG--PFSVECDIADBADVLKIVEAVKRALMVYG 558  
 QY 762 DYKESWRLQERGMSCDPSFWEHALEYDVL 793  
 DB 559 --TPAFEMTQNCMAQDLSSWKPAAKMEKFL 588

## RESULT 15

US-10-272-291-3  
 ; Sequence 3, Application US/102722291  
 ; Publication No. US20030150023A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Exseed Genetics  
 ; TITLE OF INVENTION: Starch  
 ; FILE REFERENCE:  
 ; CURRENT APPLICATION NUMBER: US/10/272,291  
 ; CURRENT FILING DATE: 2002-10-17  
 ; PRIOR APPLICATION NUMBER: 60/329,525  
 ; PRIOR FILING DATE: 2001-10-01  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 600  
 ; TYPE: PRT  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: wild type EX385 sequence  
 ; US-10-272-291-3

Query Match 20.3%; Score 869; DB 12; Length 600;  
 Best Local Similarity 40.6%; Pred. No. 8.9e-60;  
 Matches 208; Conservative 70; Mismatches 198; Indels 36; Gaps 11;

QY 308 MNVVVVAACSPMCKTGGIGDVGALPKALAKRGHRVWVVRVYGDYEADVGRKYYK 367  
 DB 77 MNVVFVGAEMAPMSKTGGIGDVGGLPPMAANGHRVWVVRVYQYDAMDTSVSEIK 136  
 QY 368 AAGQDEWVYFAYIDGVFVIDAPLFRH-----QEDTY-----GSGROEMIKRMILFC 418  
 DB 137 MDGYETVAFHFCYKRGVDRVFDHPLFLKVMGKTKIYGPVAGTIDYRQQLFSLIC 196  
 QY 419 KAAVEPWHVPCGVPGD---NLVFANDMHTALLPVYLKAYRDHGLMQYTRSLMV 474  
 DB 197 QALAEPRILSNNNDYFSGPYGDEYFVFCMDMHTGPISSCYKSNYQSHGIYRDAKTAFC 256  
 QY 475 IHNIAHQGRPVDEFPFTELEHLEHRLVD---PVGSHANYFAAGLRKADQVVVVS 530  
 DB 257 IHNISQGRFAPSDYDELNLPFRFSSFDFTDGYEKPEVGRKIMMKAGILEADRVLYL 316  
 QY 531 PGYIMELKT-VEGWSGLHDIIRQNDMKTREGIVNGIDNMENPDEVVHLKSDGYTNFSLG 589  
 DB 317 PYYAELLSIGIARGCGLDNIIMELTG--ITGIYNGMDVSEWDSRDKYLA---VYCDVST 370  
 QY 590 LBSGRCKEKLQRELGQVADVPILGTLGRDQKGVETIADAMPWIVS--QDVQVLM 647  
 DB 371 AVEAKALNKEALQAEVGLPVDNITPLVAFITGLEEQKGVVAAALPOLMEVVEDVQIVL 430  
 QY 648 LGTRHDLSMLHFEREHNDKYRGWVGESVRLARITAGADALIMSPREPCGLNOLYAM 707  
 DB 431 LGTGKKKFERMLMSAEKFPKGVRAVVKFNALAHINAGADVLAIVTSRFBFGGLIQLQG 490

Mon Feb 23 11:51:13 2004

us-10-018-418-4.rabb

Page 10

QY 708 M A G T A V E V N H A V G S V D I T V P P P P F N H S L ----- G M T F D R A E A H K L I A L C H C I R T Y R D - 7622

Db 491 M R G T P A C A C A S T G I L V D T I I E G T G F P H M R L S V D C N V E P A D V K V A T T L O R A I K V V G T P 550

QY 763 - Y K S W R G L Q E R G M S D F S E H E A K L Y E D V L L 793

Db 551 A Y E M V N C --- M I D L S W K G P A K M E N V L L 578

Search completed: February 20, 2004, 11:18:29  
Job time : 40 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 20, 2004, 11:09:27 ; Search time 21 Seconds  
(without alignments)

3658.989 Million cell updates/sec

Title: US-10-018-418-4

Perfect score: 4276

Sequence: 1 MSSAVASASFLALASAPG.....SWEHAATYEDVILKAYCW 799

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0 %  
Maximum Match 100 %  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2811.5	65.8	732	2	T01208 starch synthase (E
2	2642	61.8	491	2	T06798 probable starch sy
3	2314.5	54.1	698	2	T01209 starch synthase (E
4	2146	50.2	752	2	S61505 glycogen(starch) s
5	2028.5	47.4	786	2	T07667 glycogen(starch) s
6	1176	27.5	641	2	T07668 starch synthase (E
7	1127.5	26.4	610	2	T06280 probable starch sy
8	1071	25.0	622	2	T06280 starch synthase (E
9	1060	24.8	626	2	J02322 starch synthase (E
10	1056	22.7	322	2	T07924 S43341 probab
11	948	22.4	608	2	T07924 starch sy
12	910	21.3	608	2	T10906 starch synthase (E
13	908	21.2	610	2	F66453 granule-bound star
14	903	21.1	603	2	S61504 glycogen(starch) s
15	903	21.1	607	1	YDPOY starch synthase (E
16	883	20.7	608	2	T14731 glycogen(starch) s
17	880	20.6	615	1	YDWTY glycogen(starch) s
18	875.5	20.5	603	1	YUBHY glycogen(starch) s
19	873	20.4	609	2	J00703 glycogen(starch) s
20	869	20.3	605	1	S07314 glycogen(starch) s
21	862	20.2	609	2	S11481 glycogen(starch) s
22	770	18.0	486	2	H73221 glycogen synthase
23	765.5	17.9	477	2	B95130 starch synthase (E
24	764.5	17.9	477	2	H98000 starch synthase (E
25	717	16.8	483	2	C86712 starch synthase (E
26	713.5	16.7	484	2	S40051 starch synthase (E
27	686.5	16.1	472	2	A13040 glycogen synthase
28	681	15.9	476	2	E83785 starch (bacterial
29	675	15.8	477	2	A97176 glycogen synthase,

30	652	15.2	484	2	F82165 glycogen synthase
31	638	14.9	477	2	A10995 starch synthase (E
32	633	14.8	477	2	S76496 hypothetical prote
33	624.5	14.6	480	2	AF3057 glycogen synthase
34	624.5	14.6	480	2	H98228 glycogen synthase
35	604	14.1	477	1	SYECGL starch synthase (E
36	604	14.1	477	2	B98163 glycogen synthase
37	604	14.1	477	2	C86009 glycogen synthase
38	603.5	14.1	486	2	C36018 probable starch sy
39	603	14.1	530	2	AH3194 glycogen synthase
40	600.5	14.0	491	2	S74473 probable starch sy
41	599	14.0	476	2	AE0479 starch synthase (E
42	589	13.8	492	2	AG1810 glycogen (starch)
43	574.5	13.4	463	2	C70363 glycogen synthase
44	573	13.4	1071	2	T04926 starch synthase ho
45	555.5	13.0	1025	2	H86250 hypothetical prote

## ALIGNMENTS

## RESULT 1

T01208 starch synthase (EC 2.4.1.21) isoform STSII-1 - maize (fragment)

N;Alternate names: starch synthase isoform STSII-1  
C;Species: Zea mays (maize)  
C;Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 16-Aug-2000

C;Accession: T01208

R;Knight, M.E.; Ham, C.; Lilley, C.E.R.; Guen, H.P.; Singletary, G.W.; Mu-Forester, C

Plant J. 14, 613-622, 1998

A;Title: Molecular cloning of starch synthase I from maize (W64A) endosperm and expres

A;Reference number: Z14279; PMID:98340555; PMID:9675904

A;Accession: T01208

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-732 <NN>

A;Cross-references: EMBL:AF019296; NID:G281133; PIDN:ADD13341.1; PID:G2655029

A;Experimental source: strain W64A; endosperm

C;Genetics:

A;Gene: SSIIa

C;Function:

A;Description: catalyzes the alpha-1,4-glucosylation of starch by ADPGlucose producing

C;Superfamily: starch synthase

C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 65.8%; Score 2811.5; DB 2; Length 732;

Best Local Similarity 68.2%; Pred. No. 1.3e-158;

Matches 550; Conservative 58; Mismatches 116; Indels 83; Gaps 10;

QY	1	MSSAVASAS-----FLALASAPGRSRRARVAGPPHAGAG--LHMPWPQRTADGG	55
DB	1	MSSAAVSSSSSTFFLALASAPG-GRRAKVGSSSPFHGASLFAFMAPSPAPRDA	59
QY	56	V--AAAPAKKQARVDDDAASARQPPARRGATVAERDPVKTLDRAEGAPAPPA	113
DB	60	LVAAAEAGAGKAPRPSGDAARLPRARNA---VSKRRDPLQ-----	99
QY	114	PRDDARPPSMGCTPVNGENKSTGGGATKSGLPAPAPRPSQNRVPVNGENKANYA	173
DB	100	-----PVRGYSATGN-----TARTGAASCONMALADVELKSIYA	134
QY	174	SPPTSAIEVAPDASATISIDKAPESVVPLEKPPSSGGSNFVASAPRDLDSDEBE	233
DB	135	APPTSIKTPAPCYRMILPSGDIAPETVPAPKPLHES-----PAVDGDSN----	180
QY	234	LKKGATVVEAPRKLSPPA--PAVQEDLMPEKKYIGSEEPVEAKDQSMVAADAGSPE	292
DB	181	-----GIAPTVPELVQEAFTWPKYIGFDEDEAKDSRVGADDSGSE	225
QY	293	HHQNDGSLAGENVVNVVAAECSPWCKTGLGPAVALPKALAKRGHVMVVPYRG	352
DB	226	HYDNDGSLAGENVVNVVAAECSPWCKTGLGPAVALPKALAKRGHVMVVPYRG	285

QY	353	DYEADVDVRRKXKYKKAAGDMENVNFHAYIIGVDFVTDAPLFRHROEDITYGSGRQEI	412
Db	286	DYEADVDMDGIRKXKYKKAAGDLEVNFFHAFIDGVDFVTDAPLFRHRODDITYGSGRQEI	345
QY	413	RMLLFCKAAYEPMHVPVPCGGVPGDGNVFIANDMHTLLPYTKAYYRHHGMQYTSI	472
Db	346	RMLLFCKAAYEPMHVPVPCGGVCGGAGVFIANDMHTLLPYTKAYYRHHGMQYTSV	405
QY	473	MTIHNIHAOGRGVDPEFPTELPEHYLHFRLYDPVGGEHANYPAAGLKXADVVVVSQ	532
Db	406	LVTHNIHAOGRGVDPEFPYMDLPEHYHOFELYPVGGEHANIYPAALKXADRVTVVSRG	465
QY	533	YLVELKTVGGGMDHIIIRONDMKRGVINGIDMNMENPEVDYLSKDGTFNSLGTLS	592
Db	466	YLVELKTVGGGMDHIIISNDMKINGIYNGIDHGMKPDYLRSDGTINSLSTLDA	525
QY	593	GKQCKEALORELGLVLRADVPILCFIGRLDSQKVEIADAMFWVSODVULVMLGTGR	652
Db	526	GKQCKEALARELGLVLRDVPILCFIRLDSQKGVLDIGAMFWINGDVOULVMLGTGR	585
QY	653	HDLESLRHFEREHHDKVGMVGSFVRLAHRITTAGADALMPSPFPCGIMOLYAMA	712
Db	586	ADLEBRLQHLERHHPKXVGMVGSFVPMANHITAGADVLVWSPFPCGIMOLYMA	645
QY	713	VPPVHAAGVGRDVPPEPDPFNHSGIGMTFDRAEAKLIEALGHGLRTYDYKES	772
Db	646	VPPVHAAGVGRDVAPEPDPGAGIGMTFDRAEANKLIEALRHCLDITYRCKG	705
QY	773	RGMQDSFWEHAKLYEDVTLKAKQW 799	
Db	706	RGMQDLSWDHAEIYEDVLYAKQW 732	
RESULT 2			
T06798			
Probable starch synthase (EC 2.4.1.-) - wheat (fragment)			
C/Species: Triticum aestivum (common wheat)			
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 03-Nov-2000			
C/Accession: T06798			
R/Malter, L.; Lueitcz, H.; Lueitcz, S.T.			
submitted to the EMBL Data Library, August 1996			
A/Reference number: Z15823			
A/Accession: T06798			
A/Status: preliminary; translated from GB/EMBL/DBJ			
A/Molecule type: mRNA			
A/Residues: 1-491 <WAL>			
A/Cross-references: EMBL:U6377; NID:q1620653; PIDN:AA17085.1; PID:q1620660			
A/Experimental source: cv. Florida; endosperm; 21 days after anthesis			
C/Genetics:			
A/Gene: SS1			
C/Superfamily: starch synthase			
C/Keywords: glycosyltransferase; hexosyltransferase			
Query Match			
Best Local Similarity 98.6%; Score 2642; DB 2; Length 491;			
Matches 484; Conservative 4; Mismatches 3; Indels 0; Gaps 0;			
QY	309	NNVVVAACSPMCKTGSLGDVAGALPKALARGHRVWVPRYDYEADVDVRRKXKYA	368
Db	1	NNVVVAACSPMCKTGSLGDVAGALPKALARGHRVWVPRYDYEADVDVRRKXKYA	60
QY	369	AGODMEVNFHAYIDGVDFVTDAPLFRHROEDITYGSGRQEI	428
Db	61	AGODMEVNFHAYIDGVDFVTDAPLFRHROEDITYGSGRQEI	120
QY	429	PCGGVPGDGNVFIANDMHTLLPYTKAYYRHHGMQYTSIMVHNIHAOGRG	488
Db	121	PCGGVPGDGNVFIANDMHTLLPYTKAYYRHHGMQYTSIMVHNIHAOGRG	180
QY	489	FPETELPEHYLHFRLYDPVGGEHANYPAAGLKXADVVVVSQ	548
Db	181	FPETELPEHYLHFRLYDPVGGEHANYPAAGLKXADVVVVSQ	240

Oy	I I K Q N M K R G I A N G I D N N E M P E V D L K S G Y N F E L G L D S G K O C K E A L O R E I G L Q	608
Db	241 I I I Q N D M K R G I A N G I D N N E M P E V D L K S G Y N F E L R T L D S G K O C K E A L O R E I G L Q	300
Oy	609 V R A D V P L L E F I G L D S G K O K V E I I A D A M P W I Y Q V Q L Y M L G T S H D L E S M L R H E R E R H D	668
Db	301 V R A D V P L L E F I G L D S G K O K V E I I A D A M P W I Y Q V Q L Y M L G T S H D L E S M L Q P E R E H D	360
Oy	669 K V G W G F S V R L A H R I T A G A D A L L M P S R F E P C G I N Q L Y A M A Y G T V P V H A V G Y R D V P P	728
Db	361 K V G W G F S V R L A H R I T A G A D A L L M P S R F E P C G I N Q L Y A M A Y G T V P V H A V G Y R D V P P	420
Oy	729 F D E F N S G I G M F D R E A H K L I E A L G H C L R T R D P K S E N R G L O R G M S O D P S M E H A K L Y	788
Db	421 F D E F N S G I G M F D R E A H K L I E A L G H C L R T R D P K S E N R L O R G M S O D P S M E H A K L Y	480
Oy	789 E D V L L K A K T Q W 799	
Db	481 E D V L V R A K T Q W 491	
 RESULT 3 T01209		
Starch synthase (EC 2.4.1.21) isoform STSiI-2 - maize		
NAlternate names: starch synthase isoform STSiI-2		
CSpecies: Zea mays (maize)		
CDate: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Aug-2002		
CAccession: T01209		
RKnight, M.E.; Harrn, C.; Lilley, C.E.R.; Guan, H.P.; Singletary, G.W.; Wu-Forester, C.		
Plant J. 14, 613-622, 1998		
ATitle: Molecular cloning of starch synthase I from maize (W64A) endosperm and expressed		
AReference number: Z14279; MID:198340555; PMID:9675904		
AAccession: T01209		
AStatus: translated from GB/EMBL/DDBJ		
AMolecule type: RNA		
AResidues: 1-698 <NNI>		
ACross-references: EMBL:AF019297; NID:g2655030; PIDN:AAD13342.1; PID:g2655031		
AExperimental source: strain W64A; endosperm		
AGene: SSIIb		
CFunction:		
ADescription: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose producing		
ASuperfamily: starch synthase		
CKeywords: glycosyltransferase; hexosyltransferase		
Query Match            54.1%; Score 2314.5; DB 2; Length 698; Best Local Similarity   57.9%; Pred. No. 2.9e-129; Matches 468; Conservative 76; Mismatches 145; Indels 119; Gaps 15;		
Oy	1 M S N A V S A S F L A L A S A F G S R R R A R Y S A -- P P H A G A G - R L H W P - P M P P Q T A R D G G	55
Db	1 M P A I S S S S A F L P V A S S P R R R G S Y G A L R S Y G S Y G A L R L H M A R G P Q -- D G A	56
Oy	56 V A A R A A G K D A R V D D A A -- S A R Q P R A R C G A A T K V A E R D P Y K T L D R D A E G A D A P P	112
Db	57 A S V R A A A A A P A G C S E S E A A S S S S O A G A V Q S T A K A V ----- D S A S P E N L T S	104
Oy	113 A P R Q D A A P P S M N G F P V N G E N K S T G G G A T T D S G L P A P A R P H S T G N R V P V N G E N K A N Y	172
Db	105 A P R Q ---- S G S A M Q N C --- T S G S S A S T A A P V S G - K A D H S -----	159
Oy	173 A S P F T I A E V A P D S A A N T S I S D K A P S B S V H A E K P P S S G S N F V S A S A P R L D I D S D V E P	232
Db	140 ---- A P V T K R E I D A S ----- A V K P E P A G ----- D D A R P	163
Oy	233 E L K K G A V I Y E A P N P K A L S P P A P A V Q E D L M D F K Y I F E E P V E A X D G M A V A D D A G S F E	292
Db	164 ---- V E S ----- I G I A P V D A K D A D A P T D A A S A P	190
Oy	293 H - H Q N D S P L A G E N V M V V V A A A C S P W C T T G C L G D V A G A L P K A L A K G H R V W V V P R Y	351
Db	191 Y D E N D E P P L A G P V M V M V V V A S E C A F C T T G G I G D V G A L P P A L A R R G H R V W V V I P R Y	250

QY 352 GDYEAYDVYKRYKKAAGQDMEVNYFAYIDGVDFVDAFLPFRROEDYIGSGROEIM 411  
 DB 251 GYAEARBDLQRRRRKVAQDSEVYVYFHSYIDGVDFVFEAPRPFHRNNIYGGRLDIL 310  
 QY 412 KXMIIFCKAAVEVPMVAPCGSVFYGDQNVLFANMWHNALLPYLKAYYRPHGLMOYTRS 471  
 DB 311 KXMIIFCKAAVEVPMVAPCGSVFYGDQNVLFANMWHNALLPYLKAYYRPHGLMOYTRS 370  
 QY 472 IMVYHIAHQGRGVDFEPEFTELPEHYLEHFRLYDPVGEHANYEAAQKKAQVYVVP 531  
 DB 371 VLVYHIAHQGRGVDFEPEFTELPEHYLEHFRLYDPVGEHANYEAAQKKAQVYVVP 430  
 QY 532 GYIWEIKTYEGWGLHDIIRONDWKTGIVNGIDNKNPEVDVHLKSDGYTNEBGLTD 591  
 DB 431 GYIWEIKTYEGWGLHDIIRONDWKTGIVNGIDNKNPEVDVHLKSDGYTNEBGLTD 490  
 QY 592 SGKROCKEALORELQVADVPLLGFIQRLDQCKVEIADAMPVYSQDVQVLMGTG 651  
 DB 491 TKGQCKEALQRLQVADVPLLGFIQRLDQCKVEIADAMPVYSQDVQVLMGTG 550  
 QY 652 RHDLESMLHFEHREHNDKVRGVVSVRLAHTTAGADALLMPSPREPCGLNQYAMAAG 711  
 DB 551 RADLEDMLEHREHREHNDKVRGVVSVRLAHTTAGADALLMPSPREPCGLNQYAMAAG 610  
 QY 712 TVPVYAVGVPRDTPVPPDPENHSGLGWTFDRAEAKHLEALGHCLRTYRDYKESNRGLD 771  
 DB 611 TVPVYAVGVPRDTPVPPDPENHSGLGWTFDRAEAKHLEALGHCLRTYRDYKESNRGLD 670  
 QY 772 ERGMSDFSWERHAAXLYEDVTLKAKYQW 799  
 DB 671 ARGMAEDLSWDAVAALYEDVTLKAKYQW 698

RESULT 4  
 S61505  
 glycozen(starch) synthase (EC 2.4.1.11) isoform II precursor - garden pea  
 N:Alternate names: glycozen(starch) synthase (EC 2.4.1.11) isoform II precursor; granule  
 C:Species: Pium sativum (garden pea)  
 C>Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 16-Aug-2002  
 C:Accession: S61505; S72373; S72312  
 R:Entry: Smith, A.; Edwards, A.; Bhattacharyya, M.; Dunn, P.; Martin, C.  
 Plant J. 2, 193-202, 1992  
 A:Title: Characterization of cDNAs encoding two isoforms of granule-bound starch synthase  
 A:Reference number: S61504; MUID:93251108; PMID:1302049  
 A:Accession: S61505  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-752 <DRY>  
 A:Cross-references: EMBL:X88790  
 A:Accession: S72373  
 A:Molecule type: protein  
 A:Residues: 58-59, 'H', 61-73 <DRW>  
 R:Edwards, E. A.  
 submitted to the EMBL Data Library, June 1995  
 A:Reference number: S72312  
 A:Accession: S72312

Query Match 50.2%; Score 2146; DB 2; Length 752;  
 Best Local Similarity 54.2%; Pred. No. 3e-119;  
 Matches 429; Conservative 112; Mismatches 146; Indels 104; Gaps 19;

QY 36 GAGLHMPMPMPQRTARDGVV-----ARAAGK-----DARVD-----DDAASAPRARR- 82  
 DB 39 GVGHLNC-----GSYALNHKQHVRAVGSFADENGDSQSDVDVNAIIEKSKP 87

QY 83 -----GAATKVAERDDPKTLDRDAEGAGAPAPAPQDAAPPSXNGTGVNGENKSTGG 138

DB 88 LICKNLFNNLLKERNLVSSIDSST-----PGLGEG-----NCVSESE 127  
 QY 139 GCATKDS-----GLPAPAPAPHPSTQNRVPVNGENKANVASPPTSLAEVAPASAAITIS 194  
 DB 128 KSLSRSDNPQKGLPAAVLLKP-----NG-----GTFVSNYRSKETETMAVS 170  
 QY 195 DKA-PESVVDPAEKPSPSSSGNFVYSASAPRLDSDVBEELKGAIVIEEAPPKLSP 253  
 DB 171 SVGINQCFDEIEK-----KNDVVKSS-KLEFNEQIKKL-----YERPTKDIS- 214  
 QY 254 AAPAVGEDLWDFKCYIGFEEPEAKDQGNVAVDDAGSFHHQNDSG-----PLAGENVM 308  
 DB 215 --SIRTSLSKTFENFEGANP--SKY-----VANEANFE-----SGGEKPPLAGTNM 261  
 QY 309 NVVVAACEGSPCKCTGGLGVAGALLPKALAKGHRVAVVPRGYBEAYDVGVKTYKA 368  
 DB 262 NIIIVSAECAPWSKTGGLGVAGSLPKALAFGRHVIVAPHYGNAEAADIGVRRKYV 321  
 QY 369 AGDMEVNYFAYIYDGVDFVFIAPLFRHROEDYIGSGROEIMKXMIIFCKAAVEVPMV 428  
 DB 322 AGDMEVNYFAYIYDGVDFVFIAPLFRHROEDYIGSGROEIMKXMIIFCKAAVEVPMV 381  
 QY 429 PCGGVPYGDNLVFIANDMHTALLPYLKAYYRPHGLMOYTRSIMVYHIAHQGRGVDE 488  
 DB 382 PCGGICVGDNLVFIANDMHTALLPYLKAYYRPHGLMOYTRSIMVYHIAHQGRGVDE 441  
 QY 489 FPFLEHREHLEHFRLYDPVGEHANYEAAQKKAQVYVVP 548  
 DB 442 FNTVLSGNYIDLFKMTDPVGEHANYEAAQKKAQVYVVP 501  
 QY 549 IIRONDWKTGIVNGIDNKNPEVDVHLKSDGYTNEBGLTD 608  
 DB 502 IIRONDWKTGIVNGIDNKNPEVDVHLKSDGYTNEBGLTD 561  
 QY 609 VRADVPPLGFIQRLDQCKVEIADAMPVYSQDVQVLMGTG 668  
 DB 562 VREVPPLISFGRLDHKGVDLAEALPMWMSHVQVLMGTGADLEOMLKEFEACHD 621  
 QY 669 KVRGVSVYRLAHTTAGADALLMPSPREPCGLNQYAMAAGTVPVYAVGVPRDTPV 728  
 DB 622 KIRBWSGVSVMAHRIAGSDIILMPSPREPCGLNQYAMAAGTVPVYAVGVPRDTPV 681  
 QY 729 FDPFRHSGLGWTFDRAEAKHLEALGHCLRTYRDYKESNRGLD 788  
 DB 682 FNPFRHSGLGWTFDRAEAKHLEALGHCLRTYRDYKESNRGLD 741

QY 789 EDVTLKAKYQW 799  
 DB 742 EGVTLKAKYQW 752

RESULT 5  
 T07667  
 glycozen(starch) synthase (EC 2.4.1.11) precursor (clone GT11) - potato (fragment)  
 N:Alternate names: glycozen(starch) synthase  
 C:Species: Solanum tuberosum (potato)  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 16-Aug-2002  
 C:Accession: T07667  
 R:Edwards, E. A.; Marshall, J.; Sidebottom, C.; Visser, R.G.F.; Smith, A.M.; Martin, C.  
 Plant J. 8, 283-294, 1995  
 A:Title: Biochemical and molecular characterization of a novel starch synthase from pot  
 A:Reference number: Z16079; MUID:95400340; PMID:7670507  
 A:Accession: T07667  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-788 <EDW>  
 A:Cross-references: EMBL:X87988; NID:9887648; PIDN:CA61241.1; PID:9887649  
 A:Experimental source: cv. Désirée, tuber  
 C:Comments: This protein is present both in the stroma of the plastid and tightly bound  
 C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 47.4%; Score 2028.5; DB 2; Length 788;  
 Best Local Similarity 52.4%; Pred. No. 2.8e-112;

Matches 406; Conservative 107; Mismatches 197; Indels 65; Gaps 12;

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Qy 45 WPPOR---TARDGGVAAABAAGKQARVDDDAASAROPRARGGAATVARERPVTLOR 101
Db 59 WRNRVYKATGENSEEASADESND-IGVTIEKSKYLAQODLLQOIAIRKRYYSIKS 117
Qy 102 DAA-----EGGADA-----PPAPRODAAPPSKNGTVPNGENKSTGGGATKDSGLPA 149
Db 118 SLNAKGTVDGSGSLSDVDIPVDKDYNTVTPSTATGTLTDVXNT-----164
Qy 150 PARAPHSTONRVVNGENKNAVSPPTSLAEVAPPSAETISIDAPSPSVPAKPP 209
Db 165 PPAISHDPSKREIK-RDLADERAPPUSRSITA-SSQISSTVSKRTIN-VPEETPKS 221
Qy 210 SSGSNFVVSASAPRLIDID---SDVEPELKKGAVIEAPNPALSPPAAPVQEDLMDF 265
Db 222 SQETLLDVNSRKSLVDVPGKKIQSYMPSLRKESASHVEQORNTLESGSAEANEET----277
Qy 266 KKYTGFEPPVAKDDGMAVADDAAGSFHHQNDGSPLAGENVMVNVVVAAGSPWCKTG 325
Db 278 -----EDPVNI-----DEKPPLAGTNVMTITLVASECAPMSKTKG 313
Qy 326 LGDVAAGALPKALAKRGHRVWVVPVRYGDYEAYDVGRKYYKKAQDMEVNYTHAYIDV 385
Db 314 LGDVAAGALPKALAKRGHRVWVVPVRYDNPYPERODSGVRIKYVDGQDVATYFQALLMDC 373
Qy 386 DFWITDAFLFHRQEDIIYSGSRQETMKRMILFCRAAVEVPMHVPCCGVPPYGGDNLVPIAN 445
Db 374 DFWIHSMEFRHIGNNYGNRVVDILKRMVLFCCRAALEVPMHVPCCGVPPYGGDNLVPIAN 433
Qy 446 DMHTALLFVYLKAYYRDHGLMQYTRSIVNINIAHQGRGPDEPFTELEHLYEHRLY 505
Db 434 DMHTALLFVYLKAYYRDHGLMQYTRSIVNINIAHQGRGPDEPFTELEHLYEHRLY 493
Qy 506 DPGVEERANYPAGLKMADQVNVVSPGYLMEKLTVEGGMGHDIIRONDKTKRTGYNVIGD 565
Db 494 DPGVEERANYPAGLKMADQVNVVSPGYLMEKLTVEGGMGHDIIRONDKTKRTGYNVIGD 553
Qy 566 NMENPEVVDVH-KSDGYTNFSLGTLDGSKQCKEALORELGLQVRADVPLFSGTIGLDG 624
Db 554 TKEMPELDVHPRSDGYTNFSLGTLDGSKQCKEALORELGLQVRADVPLFSGTIGLDG 613
Qy 625 QKGEVITADAMPWIVSQDVQVLMGTGHHDLBSMLRFRERHNDKRWGVGSFVRLARI 684
Db 614 QKGVLLIAEAVFMMQGVQVLMGTGRRDLQMLRQFCOHNDKRWGVGSFVRLARI 673
Qy 685 TAGADALLMPSRFEPCGILNOLYAMAYGVTPVHAAGVADVPPEPDENHSGLGMTPDRA 744
Db 674 TAGADALLMPSRFEPCGILNOLYAMAYGVTPVHAAGVADVPPEPDENHSGLGMTPDRA 733
Qy 745 EAHKILIALGHCLRTYDYKESWRLQERGSODESWHAALKYEDVLLKAKYOM 799
Db 734 EASQILIPRINCLITVREYKESWEGIQTRCMTQDLSMDNAQNAEYVLLAKYOM 788

```

## RESULT 6

starch synthase (EC 2.4.1.21) SST precursor - potato

C/Species: Solanum tuberosum (potato)

C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 16-Aug-2002

C/Accession: T07668

R:Abel, G.J.W.

submitted to the EMBL Data Library, January 1997

A/Reference number: Z16081

A/Accession: T07668

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-641 <ABE>

A/Cross-references: EMBL:Y10416

A/Experimental source: cv. Desiree; leaf

C/Genetics:

A/Genes: SSI

C/Function:

A/Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose producing  
A/pathway: starch synthase  
C/Superfamily: starch synthase  
C/Keywords: glycosyltransferase; hexosyltransferase

Query Match 27.5%; Score 1176; DB 2; Length 641;

Best Local Similarity 45.2%; Pred. No. 5.3e-62;

Matches 250; Conservative 72; Mismatches 181; Indels 50; Gaps 12;

```

Qy 283 AVADAGSFHHQ--NHDSGLAGEN-----VNVVVVVAAGSPWCKTGGLDVA 330
Db 94 SVAGDANVESHDIANDRDLSDETEMEETPIKLFENITFTAAAPYSKTGGLDVC 153
Qy 331 GALPKALAKRGHRVWVVPVRY-----GDYEAYDVGRKYYKKAQDMEVNYTHAYID 383
Db 154 GSLPKALAKRGHRVWVVPVRYLNGGSPDEKTAANVDLVPAVTHCFGDQAEVAYHEYRA 213
Qy 384 GVDFFVFDAPLFRH---SQEDIYG--GSRQETMKRMILFCRAAVEVPMHVPCCGVPPYGDG 438
Db 214 GVDWVFDHSSYCRGPTGYDYGAFGDNQ---FRFTLSHAACEAPLVPLGGFTYGE- 269
Qy 439 NLVFTANDMHTALLFVYLKAYYRDHGLMQYTRSIVNINIAHQGRGPDEPFTELEHLY 498
Db 270 KCLFLANDMHTALLFVYLKAYYRDHGLMQYTRSIVNINIAHQGRGPDEPFTELEHLY 329
Qy 499 LEHFLYDVPV-----GSEHANYFAAGLKMADQVNVVSPGYLMEKLTVEGGMGHDI 550
Db 330 YGAVEMIRPYTARALDGTETVNVTLKALINADRIILVSGYSWEITPEGGVGLHELL 389
Qy 551 RQNDKTKRTGYNVIGDMEPEVDVHLKSDGYTNFSLGTLDGSKQCKEALORELGLQVR 610
Db 390 SSRQSLVNGITIGDVMNMPNSTDEHIAS---HISINDL-SGRQCKTDLQKEIGLPIR 444
Qy 611 ADVPLIFGTRLDGQKGEITADAMPWIVSQDVQVLMGTGRRDLBSMLRFRERHNDKV 670
Db 445 EDCPLIFGTRLDGQKGEITADAMPWIVSQDVQVLMGTGRRDLBSMLRFRERHNDKV 504
Qy 671 RQWVGSVRLARITAGADALLMPSRFEPCGILNOLYAMAYGVTPVHAAGVADVPPEPD 730
Db 505 RAMVGSVNVVSHRITAGCDIILMPSRFEPCGILNOLYAMAYGVTPVHAAGVADVPPEPD 564
Qy 731 PENHSGL-----GMTDRAEHLGLCLRTYDYKESWRLQERGSODESWHAALKYEDV 786
Db 565 PTAQSGIGGTMTSPLTSEKLTDLTKALGTTYTEHKSNEGLMRKMGADYSNENAI 624
Qy 787 LYEDVLLKAKYOM 799
Db 625 QYEQV-----FTW 632

```

## RESULT 7

probable starch synthase (EC 2.4.1.21) precursor - wheat (fragment)

N/Alternate names: starch synthase

C/Species: Triticum aestivum (common wheat)

C/Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 16-Aug-2002

C/Accession: T06280

R:Block, M.; Loefer, H.; Luetticke, S.

submitted to the EMBL Data Library, February 1996

A/Reference number: Z15585

A/Accession: T06280

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-610 <BLO>

A/Cross-references: EMBL:U48227; NID:g1373145; PIDN:AA802197.1; PID:g1373150

A/Experimental source: cv. Florida, endosperm of kernels

C/Function:

A/Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose producing

C/Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match

Best Local Similarity 26.4%; Score 1127.5; DB 2; Length 610;

Matches 235; Conservative 69; Mismatches 156; Indels 27; Gaps 9;





QY 118 AARPESM---NGTPVNGENKSTGGGATDGLPAPAPAPHPSTONRVVNGENKANYAS 174  
 DB 57 QPVLPTFLVPTSTP-----PAPTOSAPAA----- 80  
 QY 175 PPTISLEAVAPDAATISISDKAPESVPAKPPSSGSGNFVYASAPRLIDSDVESEL 234  
 DB 81 -----PTPELPDSGV-----GELEBDL 98  
 QY 235 KKGAVIVEAPNPKALSPAPAPVQEDLDFKKYICFEEPEVAKDGMVADADGAFEH 294  
 DB 99 E-----GLTEDSIDKTIFFVASEQSESEIMD-----YKSOA----- 127  
 QY 295 QNHDSGLAGENMNVVVAAGSPMCKTGGLGDVAGALPKALAKRGHEVMVPRY--- 351  
 DB 128 -----QAKVTRSVFTTGEASPYAKSGGLGDVCGSLPINALRGHEVMVPRYNG 179  
 QY 352 ---GDYBEADVGVKXYKKAAGDMENVYFAVIDGVDFIDAPLFRHGOEDIG--G 405  
 DB 180 ALMKNFANAFYTEKHIKIPCFGGEHEWTFPEHYRDSVDWVFDHPSY-HRPGNLXGDNFG 238  
 QY 406 SROEIMGRMLTFCFAVEVMHVPCCGVPYGDGNLVIANDMTALLPYLKAHYADHGL 465  
 DB 239 AFGNQRYTLTLCACAPLILIELGTYIG-KCMFVNDWASLVPVILAAKTRPYGV 297  
 QY 466 MQYTRSLMTVHNIAHOGRGVDEPFTLEPHYL-----EHFRLYDPVGEHANYTA 517  
 DB 298 YRDARSVLVHNLAHGVEPASTYPLDGLPPEWGALEWVPEMARHALLDKGEAVNPLK 357  
 QY 518 AGLKMAQVYVVSQYIMELKTYEGGGLHDIIRONDWKRGVINGDMMENPEVDYL 577  
 DB 358 GAVVTAIRIVVSGGYMEVVTAGGGGLNELSSKASVINGVNGIDINDMNPSTDKL 417  
 QY 578 KSDGYTFSLGTLDSGRQCKEALQRELGQVADVPLLFIRLDQCKVEIADAMP 637  
 DB 418 P-----YHYSVDL-SGAKKCAELQKELGPIRDVPLIGFGLDYOKSIDILKIALPD 472  
 QY 638 IVSODVQVLMGTGRHLESLRPFREHDKATGNGVSLAHTTAQADLLMPSRF 697  
 DB 473 LMRNINQFVLMGSDPGEFGMRSTESGYRDKFGWGSVPVSHRIIACDILLMPSRF 532  
 QY 698 EPCGLNLYAMAYGTPVVAHVGVRDVPFPDF--NHSGLGMP 741  
 DB 533 EPCGLNLYAMQYGVVPHGTGLRDRIVENFNFAEKGEQGTMAF 579

## RESULT 10

T07924  
 Probable starch synthase (EC 2.4.1.-) - Chlamydomonas reinhardtii (fragment)  
 C:Species: Chlamydomonas reinhardtii  
 C:Date: 21-May-1999 #sequence\_revision 21-May-1999 #text\_change 03-Nov-2000  
 C:Accession: T07924  
 R:D'Haese, C.; Abel, G.; Kossmann, J.; Ball, S.  
 submitted to the EMBL Data Library, September 1997  
 A:Description: Cloning of cDNAs coding for starch synthases in the green algae Chlamydomonas reinhardtii  
 A:Reference number: Z16218  
 A:Accession: T07924  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-332 <DHU>  
 A:Cross-references: EMBL:AF026421; NID:g3169786; PIND:AA017970.1; PID:g3169787  
 A:Experimental source: strain 137C; clone CD191  
 A:Superfamily: starch synthase  
 C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 24.7%; Score 1056; DB 2; Length 322;  
 Best Local Similarity 60.2%; Pred. No. 2, 7e-55;  
 Matches 192; Conservative 49; Mismatches 78; Indels 0; Gaps 0;  
 QY 481 OGRGVPDEPFTLEPHYLPHRLYDPVCGEHANTFPAAGLAKADQVYVVSQYIMELKTY 540  
 DB 4 RGGPVESEHLEINFEYRERFRLLYDPIGSEHNVKKGALBCAHLVAVVSKCYAMECQT 63

QY 541 EGGNGLHDIIRONDWKTRGIVNGIDNMENPEVDYALKSDGYTNSJGLTDSGRQCKEA 600  
 DB 64 EGGNGLHEVIAKVNMLRGVINGIDYKEMNPIDDEFLLTDDYAHYVDPTLAGKACKRA 123  
 QY 601 LQRELQVADVPPLGIFGLDQCKVEIADAMWITSQDVOLMTGTHDSEMR 660  
 DB 124 LQRELQVADVPPLGIFGLDQCKVEIADAMWITSQDVOLMTGTHDSEMR 183  
 QY 661 HFERHDKVRGWGSESVRLAHRITAGADALIMPSRFPGLNOLYAMAYGVTPVVAVG 720  
 DB 184 DMENRNKQCGRWGSESVRLAHRITAGADALIMPSRFPGLNOLYAMAYGVTPVVAVG 243  
 QY 721 GVRDTPPPPPFNSHSGIWTFFDRAEAKLIELGHCLRTYDVKESMRGLQERGMQDF 780  
 DB 244 GLRDTVQYSPFENVGVGWFEREANKLRESINNALYTRQFDSFRGQRRGMQDUT 303  
 QY 781 WEHAKLYEDVTLKAKYQW 799  
 DB 304 WDNAASIEBYLVAAKYQW 322

## RESULT 11

S43341  
 search synthase (EC 2.4.1.21) precursor - cassava  
 N:Alternate names: bacterial-glycogen synthase; glycogen synthase; starch synthase  
 C:Species: Manihot esculenta (cassava)  
 C:Date: 07-Sep-1994 #sequence\_revision 03-Nov-1995 #text\_change 16-Aug-2002  
 C:Accession: S43341  
 R:Salehuzzaman, S.N.I.M.; Jacobsen, E.; Visser, R.G.F.  
 Plant Mol. Biol. 23, 947-962, 1993  
 A:Title: Isolation and characterization of a cDNA encoding granule-bound starch synthase  
 A:Reference number: S43341; MUID:94083565; PMID:8260633  
 A:Accession: S43341  
 A:Molecule type: mRNA  
 A:Residues: 1-608 <SLA>  
 A:Cross-references: EMBL:X74160; NID:9437041; PIND:CA52273.1; PID:9437042  
 A:Gene: GBS1; waxy  
 A:Genome: nuclear  
 C:Function: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose producing  
 A:Superfamily: starch synthase  
 C:Keywords: amyloplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltran-  
 F:1-78/Domain: transit peptide (amyloplast) #status predicted <TMP>  
 F:79-608/Product: ADPglucose-starch glucosyltransferase #status predicted <MAT>

Query Match 22.2%; Score 948; DB 2; Length 608;  
 Best Local Similarity 41.5%; Pred. No. 1, 5e-48;  
 Matches 216; Conservative 77; Mismatches 172; Indels 56; Gaps 12;

QY 308 NNVVVVAACSWCKTGIGDYAGALPKALAKGRHNVVPRVGDYEADVGRKXYK 367  
 DB 82 NMLIFGAEVGPWSKTGIGDYAGALPKALAKGRHNVVPRVGDYEADVGRKXYK 141  
 QY 368 AAGDMEVYFPAVIDGVDFIDAPLFRHGOEDIG--GSR-----QELTKMT 415  
 DB 142 IGDRIETVAFHSYKRGVDRVVDHMF---LEKWKGTGSKTYGPRAGLDVQDQLRFS 198  
 QY 416 LFCRAVEVPMHVPCCGV-----PYGDGNLVTIANDMTALLPYLKAHYRHHGMQYR 470  
 DB 199 LFCRAVEVPMHVPCCGV-----PYGDGNLVTIANDMTALLPYLKAHYRHHGMQYR 257  
 QY 471 SIWVHNIAHOGRGVDEPFTLEPHYLPHRLYD-----PVGGEHANYFAAGLAKADQV 526  
 DB 258 VAFCHINIAHOGRGVDEPFTLEPHYLPHRLYD-----PVGGEHANYFAAGLAKADQV 317  
 QY 527 VVVSQYIMELKTYEGGGLHDIIRONDWKTRGIVNGIDNMENPEVDYALKSDGYTNS 585  
 DB 318 LTVSPYAAQVIGISVGRVGLDNFIRKTG--TAGIINGMDVQEMNPVVDKYTD---IHY 371  
 QY 586 SLGTLDSGRQCKEALQRELGQVADVPLIGFGLDQCKVEIADAMPVIVSODVQL 645  
 DB 372 DATVMDAKFLKEALQAEVGLPVDRNVPLIGFGLDQCKVEIADAMPVIVSODVQL 431

QY 646 VMLGTRHDIKESMLRFREREHNDKVGWGVFSRLAHRITAGADALIMSPREPCGINOL 705  
 DB 432 VILGTGKKKFKKXKJIEHLVLYPDKARGVAKFNVPALHMITAGADFMVLVSPREPCGLIOL 491  
 QY 706 YAMAGTVPVVAHVAGVGRDTPVPEFDPFNHSGLGWT-----FDRAEAHKLIEA 752  
 DB 492 HAMRGTVPIVASTGGLVNTVKE-----GYTFQMGALHVECDKIDSADVAIVK 542  
 QY 753 LGHCLRTYRDYKESWGLQERGMQSPFSWEHAAKLYEDVLL 793  
 DB 543 VARALGTIVA--TAALREMLINCAODLSWKGPARMEKXLL 581

## RESULT 12

T10906  
 starch synthase (EC 2.4.1.21) - sweet potato  
 N/Alternate names: starch synthase  
 C/Species: Ipomoea batatas (sweet potato)  
 C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Aug-2002  
 C/Accession: T10906  
 R/Mang, S.J.; Yeh, K.W.; Tsai, C.Y.  
 submitted to the EMBL Data Library, December 1995  
 A/Reference number: Z17212  
 A/Accession: T10906  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-608 <MAN>  
 A/Cross-references: EMBL:U44126; NID:G1172158; PID:G1172159  
 A/Experimental source: cv. Tainong; tuberous root  
 C/Genetics:  
 A/Gene: SS67  
 C/Function:  
 A/Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose producing  
 A/Pathway: starch biosynthesis  
 C/Superfamily: starch synthase  
 C/Keywords: glycogen/starch biosynthesis; glucosyltransferase; hexosyltransferase

## Query Match

Best Local Similarity 21.3%; Score 910; DB 2; Length 608;  
 Matches 214; Conservative 70; Mismatches 190; Indels 38; Gaps 11;

QY 308 MNVVVVAAGSPWCKTGGLDVGALPKALAKGHRVYVVPYRGYEAAYDVGVKRYK 367  
 DB 82 MNLVFVGCBBGPKCTGGLDVLGGLPPALAAHRMYVCPRYDYKDAWCVVVERQ 141  
 QY 368 AAGDMEVNYFAVYIDGVDFVTDAPLFRHROEDYGG-SGR-----GEIMKMT 415  
 DB 142 VGDRIEPRFPHSYKRGVDVDFVDPMF---LEKVMGKTSMLYGPYKAGDYKDNOLRFS 198  
 QY 416 LFCRAAEVPMHVCAGV-----PYGDNLVFIANDHTALLPYLKAAYRDHGLMQYTR 470  
 DB 199 LFCRAAEVPMHVCAGV-----PYGDNLVFIANDHTALLPYLKAAYRDHGLMQYTR 470  
 QY 471 SIMVHNIAHQGRGVDFEPTLPEHYLHEFLYD---PVGSEHANYFAAGLKADQV 526  
 DB 258 VAFCHINIAVQGRFASDFSLNLPDEYKGSFDFIDGDKVQKRIKMMKAGIREADRV 317  
 QY 527 VVSGPYGIMEL-KTYEGGWSGLHDIIRQNDKTRIGTVGIDMMENPEVDVHLKSDGYTF 565  
 DB 318 FTVPBNVAKELVSCSKVELELDNHR--DCGITYICMGMDQENPAPTDKFLA---VKY 371  
 QY 586 SLGLTDSGRCKEALQRELGLQVADVPLGLFTGLDQKGVIIADAMPVIVSDVOL 645  
 DB 372 DITVMAKPLKELKALQAAVGLPVDNRNPLIGTIGRLBEQKGSILVAALSKFIMDVOL 431  
 QY 646 VMLGTRHDIKESMLRFREREHNDKVGWGVFSRLAHRITAGADALIMSPREPCGINOL 705  
 DB 432 VILGTGKKKFKKXKJIEHLVLYPDKARGVAKFNVPALHMITAGADFMVLVSPREPCGLIOL 491  
 QY 706 YAMAGTVPVVAHVAGVGRDTPVPEFDPFNHSGLGWT-----FDRAEAHKLIEA 752  
 DB 492 HAMRGTVPIVASTGGLVNTVKE-----GYTFQMGALHVECDKIDSADVAIVK 542  
 QY 753 LGHCLRTYRDYKESWGLQERGMQSPFSWEHAAKLYEDVLL 793  
 DB 543 VARALGTIVA--TAALREMLINCAODLSWKGPARMEKXLL 581

QY 762 DYKESWGLQERGMQSPFSWEHAAKLYEDVLL 793  
 DB 552 TL--AFTEMIKCMQSLSMKGPRAKMEVLL 581

## RESULT 13

F66453

granule-bound starch synthase (imported) - Arabidopsis thaliana  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C/Accession: F66453  
 R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federzoni, N.A.; Kaul, S.; White, O.; Alonso  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.  
 ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, R.; Moore, T.; Kowles, D.; Sakano, H.  
 A/Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A/Reference number: A66141; MUID:21016719; PMID:11130712  
 A/Accession: F66453  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-610 <STO>  
 A/Cross-references: GB:A6005172; NID:96910568; PID:AAF31273.1; GSPDB:GN00141  
 C/Genetics:  
 A/Map position: 1  
 C/Superfamily: starch synthase

## Query Match

Best Local Similarity 21.2%; Score 908; DB 2; Length 610;  
 Matches 213; Conservative 80; Mismatches 209; Indels 42; Gaps 12;

QY 273 EPVEAKDGMVAVDAGSFEHONHDSGLNENNVVVVVAACSPWCKTGGLDVGAGA 332  
 DB 59 KPVSAK-----SKRSSKTKAGKIVCEKMSVIFIGALVGRMSKGGGLVIG 108  
 QY 333 LPKALAKGHRVYVVPYRGYEAAYDVGVKRYKAAQDMEVNYFAVYIDGVFVTDAPL 392  
 DB 109 LPALAAAGHRVMTICPRYDYKDAWCVVVERQKRVKENVAFPHCYKAGVDRVDFDH 168  
 QY 393 PLFRHR-----CEDYGG-----SROEIMKMTLFCRAAEVPMHVCAGV-----PYGDS 438  
 DB 169 PFLAKVVGKSGSKYGPITGVNDYNDOLRSLCQALLENPVLNINSSKXFSFGYGE 227  
 QY 439 NLVFIANDHTALLPYLKAAYRDHGLMQYTRISVHNIAHQGRGVDFEPTLPEHY 498  
 DB 228 DVVFAVANDHTALLPYLKAAYRDHGLMQYTRISVHNIAHQGRGVDFEPTLPEHY 498  
 QY 499 LEHFLYD---PVGSEHANYFAAGLKADQVYVVPYRGYEAAYDVGVKRYKAAQDMEVNYFAVYIDGVFVTDAPL 553  
 DB 288 KSPFDMQYGEKPVGKRIKMMKALIEARVLTSPFYAABELLSGVDKGYELKYLEMK 347  
 QY 554 DWKTRIGVINGIDNMENPEVDVHLKSDGYTFSLGLTDSGRCKEALQRELGLQVADV 613  
 DB 348 --TVSGIINGMDVQWNPSTDKID---IKYDITVDAKPLKELKALQAAVGLPVDADV 401  
 QY 614 PLGLFTGLDQKGVIIADAMPVIVSDVOLVMTGTRHDIKESMLRFREREHNDKVGW 673  
 DB 402 PVIGTIGRLBEQKGSILVAALSKFIMDVOLVMTGTRHDIKESMLRFREREHNDKVGW 673  
 QY 674 VGSFVRLAHRITAGADALIMSPREPCGINOLYAMAGTVPVVAHVAGVGRDTPVPEF 732  
 DB 462 AKFNVPALHMITAGADFMVLVSPREPCGLIOLHARVYGPVIVASTGGLVNTVKE 521  
 QY 733 NMSGGLTDRDAEAKLIEALGHCRTYRDYKESWGLQERGMQSPFSWEHAAKLYE 789  
 DB 522 HIGRFNVKCEVVDPDVATATAKAVTAAVAVGTS--AAQENYKNCDDPFSWKGPARLME 579  
 QY 790 DVLL 793

Db 580 KVL 583

# RESULT 14

S61504  
glycogen(starch) synthase (EC 2.4.1.11) isoform I precursor - garden pea  
N:Alternate names: glycogen(starch) synthase  
C:Species: Pisum sativum (garden pea)  
C:Date: 20-Jul-1996 #sequence\_revision 07-Feb-1997 #text\_change 16-Aug-2002  
C:Accession: S61504; S72372  
R:Dir, I.; Smith, A.; Edwards, A.; Bhattacharyya, M.; Dunn, P.; Martin, C.  
Plant J. 2, 193-202, 1992  
A:Title: Characterization of cDNAs encoding two isoforms of granule-bound starch synthase  
A:Reference number: S61504; MIMD:93251108; PMID:1302049  
A:Accession: S61504  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-603 <DR>  
A:Cross-references: EMBL:X88789; NID:9887570; PIDN:CAA61268.1; PID:9887571  
A:Accession: S72372  
A:Molecule type: protein  
A:Residues: 76-77, 'X', 79, 81-88 <DR>  
C:Superfamily: starch synthase  
C:Keywords: glycosyltransferase; hexosyltransferase  
F:1-75/Domain: signal sequence #status predicted <SIG>  
F:76-603/Product: glycogen (starch) synthase isoform I #status experimental <MAT>

Query Match 21.1%; Score 903; DB 2; Length 603;  
Best Local Similarity 39.8%; Pred. No. 6,7e-46;  
Matches 206; Conservative 84; Mismatches 179; Indels 48; Gaps 12;

QY 308 MNVYVAECSPWCKTGLDVGALPKALAKGHRVWVPRYGYEAYDVGRKYYK 367  
DB 77 MSLEVAEAVGPMVKTKGLDVGALPPLVLAGNGHRVWVSPRYDQKMDNTVAEYK 136  
QY 368 AAGDMENVYFHAVIDGVDFIDAPLFRHROEDIVG--GSR-----GEINKMI 415  
DB 137 VGDIETVRFPHCKRGVDVDFVDFLELR---VMGKTSKLYGPTGIDYDNLGRS 193  
QY 416 LFCAAEVPMHVPCCGV-----PYGDNLVFIANDMTALLPYLKAYRHDGMOYTR 470  
DB 194 LFCQAALAPRVNLNLSKTFSGGYG--DVIFANDHSHALPCYLSKMSKSLTKNAK 252  
QY 471 SIMVHNIAHQGRGVDFEFTLEPEHYLHFRLYD---PVGEHANYFAAGLKNADQV 526  
DB 253 VAFCHNIAVQGRNAFDFSLNLPDEFSSFPDIDGYNKPCGSKIMMKAGILSDQV 312  
QY 527 VVSPGYLMEKTYEG--GMGLHDIIRONDKFTKGTIVNGIDNMEWNPVVDHLKSDGYT 585  
DB 313 FTVSPHAKELISEDEGVELDNIIRSTG--IIGIVGMNDNRSESPQTDYID----VH 366  
QY 586 SLGLDSEKROCKALQRELGLQVADVPPLFGIGRLDQGVYEIIADANPMWISDQV 645  
DB 367 NETVTEKPLKLTQAEIGLPVDSPIPLIGFGRLEBQGSIIIVAAIAKADENVQ 426  
QY 646 VMLGTGRHDESMNRHFEREHNDYKRGVGSVLAHRTAGADALMPSPFPCG 701  
DB 427 VVLTGKIMKEKQLEVELEKYPGKAIGITKNSPLAKHIIAGADFIYIPSPFPCG 486  
QY 706 YAMAYGVTVVHAAGVADVP-----PDPFNHSGIAGTFDPAEALHKLIEALGHC 756  
DB 487 HAMRYGTVPIVSSIGGLVDIVYKGGTGHAGRPFVECD-----VDSDVDKLAATYKRA 541  
QY 757 LRTTRDYKESWRGLQERGMDSQFSWEHAAKLYEDVLL 793  
DB 542 LKTYG--TQAMKOIILNCAQNFMSKKPKAKLMEKALL 576

RESULT 15  
starch synthase (EC 2.4.1.21) precursor - potato  
N:Alternate names: starch synthase

C:Species: Solanum tuberosum (potato)  
C:Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 02-Aug-2002  
C:Accession: S16555; S24392; S26060; S26061  
R:van der Leij, F.R.; Vlasier, R.G.F.; Ponstein, A.S.; Jacobsen, E.; Feenstra, W.J.  
Mol. Gen. Genet. 228, 240-248, 1991  
A:Title: Sequence of the structural gene for granule-bound starch synthase of potato (S  
A:Reference number: S16555; MIMD:91360072; PMID:1886609  
A:Accession: S16555  
A:Molecule type: DNA  
A:Residues: 1-607 <LEI>  
A:Cross-references: EMBL:X58453; NID:921470; PIDN:CAA41359.1; PID:921471  
A>Note: the authors translated the codon AAC for residue 453 as Gly and GCT for residue  
A:Accession: S24392  
A:Molecule type: protein  
A:Residues: 78-92, 'X', 94-98, 'XXX', 102, 'XX', 105-107 <LE2>  
R:Ronde, W.; Becker, D.; Kull, B.; Salamin, F.  
J. Genet. Breed. 44, 311-315, 1990  
A:Title: Structural and functional analysis of two waxy gene promoters from potato.  
A:Reference number: S26060  
A:Accession: S26060  
A:Molecule type: DNA  
A:Residues: 1-43 <ROH1>  
A:Cross-references: EMBL:X52416; NID:921613; PIDN:CAA36667.1; PID:921614  
A:Experimental source: cv. Granola, clone G1  
A:Accession: S26061  
A:Molecule type: DNA  
A:Residues: 1-43 <ROH2>  
A:Cross-references: EMBL:X52417; NID:921615; PIDN:CAA36668.1; PID:921616  
A:Experimental source: cv. Granola, clone G28  
A:Gene: waxy  
A:Gene: nuclear  
A:Intron: 111/3; 138/3; 171/3; 201/3; 223/1; 256/3; 293/2; 374/3; 433/3; 526/3;  
A:Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose producing  
A:Pathway: starch biosynthesis  
C:Superfamily: starch synthase  
C:Keywords: amyloplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltrans  
F:1-77/Domain: transit peptide (amyloplast) #status predicted <TMP>  
F:78-607/Product: ADPglucose-starch glucosyltransferase #status experimental <MAT>

Query Match 21.1%; Score 903; DB 1; Length 607;  
Best Local Similarity 39.6%; Pred. No. 6.8e-46;  
Matches 208; Conservative 79; Mismatches 174; Indels 64; Gaps 13;

QY 308 MNVYVAECSPWCKTGLDVGALPKALAKGHRVWVPRYGYEAYDVGRKYYK 367  
DB 81 MNLIFVGEVGPMSKTKGLDVGALPPLAARGRVWVSPRYDQKMDNTVAEYK 140  
QY 368 AAGDMENVYFHAVIDGVDFIDAPLFRHROEDIVGSSREIN-----KRM 415  
DB 141 VGDSIEIRFPHCKRGVDVDFVDFLELR---LEKVMGTSKLYGPTGIDYDNLGRS 197  
QY 416 LFCAAEVPMHVPCCGV-----PYGDNLVFIANDMTALLPYLKAYRHDGMOYTR 470  
DB 198 LFCQAALAPRVNLNLSKTFSGPYG--DVIFANDHSHALPCYLSKMSYSGRIYNNAK 256  
QY 471 SIMVHNIAHQGRGVDFEFTLEPEHYLHFRLYD---PVGEHANYFAAGLKNADQV 526  
DB 257 VAFCHNIAVQGRNFSDFPLNLPDEFSSFPDIDGKPKKRTKIMMKAGILSDQV 316  
QY 527 VVSPGYLMEK--KTYEGGMGLHDIIRONDKFT--RGIVNGIDNMEWNPVVDHLKSDGYT 583  
DB 317 VVSPGYLMEK--KTYEGGMGLHDIIRONDKFT--RGIVNGIDNMEWNPVVDHLKSDGYT 583  
QY 584 N--FSLGLDSEKROCKALQRELGLQVADVPPLFGIGRLDQGVYEIIADANPMWISQ 641  
DB 367 DVKYDITVMAKPLKLTQAEIGLPVDSPIPLIGFGRLEBQGSIIIVAAIAKADENV 426  
QY 642 DVQVLMGTGRHDESMNRHFEREHNDYKRGVGSVLAHRTAGADALMPSPFPCG 701  
DB 427 DVQIVVLTGKKEPQGELEGLVLYPNKAKGVAAKENVLAHRTAGADALMPSPFPCG 486

Mon Feb 23 11:51:14 2004

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```
OY 702 LNOUYAMAYGTVPVVHAYGVKRVPPDPNHSGLGNT-----EDRAEAMK 748
Db 487 LIOLHAMEYGVPICASTGGLVDFVKE-----GYTGFHMGAFNVECDVVDPAADVAK 537
OY 749 LIEALGHCLRTYRDYKESMRGLOERGSODPSWEHAATYEDVLL 793
Db 538 IYTVARALAYGTL--AFAMIKNCMSSELSWKEPAKWTLL 580
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Job time : 24 secs

Mon Feb 23 11:51:14 2004

us-10-018-418-4.rsp

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 20, 2004, 11:05:48 ; Search time 17 Seconds  
(without alignments)  
2210.255 Million cell updates/sec

Title: US-10-018-418-4

Sequence: 1 MSSAVASAFPLASASP.....SWEHAKLYEDVLLKRYQW 799

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2129	49.8	752	1	UGS3_PEA
2	2028.5	47.4	788	1	UGS3_SOLU
3	1176	27.5	641	1	UGS2_SOLU
4	1175.5	27.5	652	1	UGS2_ARAT
5	1127.5	26.4	610	1	UGS2_WHEAT
6	1060	22.8	626	1	UGS2_ORYA
7	954	22.3	608	1	UGS2_ANTWA
8	948	22.2	608	1	UGS2_MANS
9	910	21.3	608	1	UGS2_IPOBA
10	908	21.2	610	1	UGS2_ARAT
11	903	21.1	603	1	UGS2_PEA
12	903	21.1	607	1	UGS2_SOLU
13	883	20.7	609	1	UGS2_SORBI
14	880	20.6	615	1	UGS2_WHEAT
15	875.5	20.5	603	1	UGS2_HORVU
16	869	20.3	605	1	UGS2_MAIZE
17	862	20.2	609	1	UGS2_ORYGL
18	862	20.2	609	1	UGS2_ORYGL
19	770	18.0	486	1	UGS2_THEMA
20	765.5	17.9	477	1	UGS2_STRN
21	714	16.7	478	1	UGS2_LACIA
22	713.5	16.7	484	1	UGS2_BACU
23	686.5	16.1	472	1	UGS2_ANASP
24	681	15.9	476	1	UGS2_BACHD
25	675	15.8	477	1	UGS2_CLOAB
26	674	15.8	485	1	UGS2_BACST
27	671	15.7	482	1	UGS2_CLOBE
28	655	15.3	461	1	UGS2_FUSUN
29	652	15.2	484	1	UGS2_VIBCH
30	643	15.0	477	1	UGS2_SALTY
31	638	14.9	477	1	UGS2_SALTY
32	633	14.8	477	1	UGS2_SALTY
33	624.5	14.6	480	1	UGS2_AGRYS

34	621	14.5	465	1	GLGA_SYNP7	Q935y7 synechococ
35	619	14.5	480	1	GLGI_RHIME	P58393 rhizobium m
36	604	14.1	477	1	GLGA_ECOLI	P08323 escherichia
37	603.5	14.1	466	1	GLG2_RHIME	P58394 rhizobium m
38	603	14.1	509	1	GLG2_AGRYS	P80438 agrobacteri
39	600.5	14.0	491	1	GLG2_SYNP3	P72623 synechocyst
40	599	14.0	476	1	GLGA_YERPE	Q82478 yersinia pe
41	589	13.8	492	1	GLG2_ANASP	Q82099 anabaena sp
42	585.5	13.7	541	1	GLGA_RALSO	Q8X773 ralsocia s
43	582.5	13.6	480	1	GLGA_PASMU	Q9C913 pasteurella
44	582.5	13.6	480	1	GLGA_RHTR	Q9C915 rhizobium t
45	578.5	13.5	481	1	GLGA_RHTR	Q985p2 rhizobium 1

## ALIGNMENTS

RESULT 1  
ID UGS3\_PEA STANDARD; PRT; 752 AA.  
AC Q43093;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Glycogen [starch] synthase, chloroplast precursor (EC 2.4.1.11)  
DE (GSSSIT) (Granule-bound starch synthase II).  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC Eucoside I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
OX NCBI\_Taxid=3888;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 58-73.  
RC STRAIN=cv. BCI/RR; TISSUE=Embryo;  
RX MEDLINE=93251108; PubMed=1302049;  
RA Dry I., Smith A., Edwards A., Bhattacharya B., Dunn P., Martin C.;  
RT "Characterization of cDNAs encoding two isoforms of granule-bound  
RT starch synthase which show differential expression in developing  
RT storage organs of pea and potato."  
RT Plant J. 2:193-202(1992).  
RL  
CC -1- CARBOLYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl) (N) =  
CC UDP + ((1,4)-alpha-D-glucosyl) (N+1).  
CC -1- PATHWAY: Starch biosynthesis.  
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST/AMTLOPLAST, SOLUBLE AND GRANULE-  
CC BOUND.  
CC -1- TISSUE SPECIFICITY: Widely expressed.  
CC -1- DEVELOPMENTAL STAGE: MOST HIGHLY EXPRESSED IN EARLY EMBRYOS.  
CC -1- SIMILARITY: Belongs to the glycosyltransferase family 1.  
CC Bacterial/plant glycogen synthase subfamily.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X88790; CAA61269.1; .  
CC PIR; S61505; S61505.  
CC InterPro: IPR001296; Glyco trans. 1.  
DR Pfam: PF00334; Glyco\_transf.1.  
DR GlycoGen biosynthesis; Transferase; Glycosyltransferase;  
KW Transmembrane; Chloroplast; Amyloplast; Starch biosynthesis.  
FT TRANSIT 1 57  
FT CHAIN 58 752  
FT BINDING 275 275  
SQ SEQUENCE 752 AA; 83617 MW; E0496420C359395 CRC64;  
Query Match 49.8%; Score 2129; DB 1; Length 752;  
Best Local Similarity 53.2%; Pred. No. 4,7e-11;  
Matches 426; Conservative 114; Mismatches 138; Indels 122; Gaps 19;

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QY 36 GAGRLHMPWPQRTARDGVA-----ARAAKCK---DARVD---DDAASARPPARRG 83
DB 39 GVGRLNC-----GSVRLNKHQHYAVAGKSGFADENGSGEDVDVATIKSKKY 87
QY 84 GAATK-----VAERDVPKTLDEDAABGGA.PAPAPRQDAARPPMNKGT.PVNGENKSTG 138
DB 88 LAIQRLEIQIARKKLVSSIDSDT-----PGLFG---NGVSESE 127
QY 139 GGATKDSGLPAPAPAPHPSTQNEVPVNGENKANA-----SPTSLAEVYA 184
DB 128 KSLSRDSE-----PGKSSSSGSAVETKRWCFQOLCRKSKETEMAV-- 169
QY 185 PDAAATISIDKAPESVAVPAEKPPSSGSFVVASAPRLDSDVEPELKKGAIVVEA 244
DB 170 ---SSVGINQODE---TEK-----KQDAVKAAS-KLHPHQIKKL-----YER 207
QY 245 PNPRLSPPAAPAVQEDLMDFKKYIGFEEFVEAKDDGMAVADAGSFEHQNHDSG--- 300
DB 208 PDKTDS-----SSIRTSILKFENEGANED-SSKE-----VANAENFE-----SGGEXP 252
QY 301 -PLAGENVNVVVAACSPWCKTGGLGVDAGALPKALAKGHRVWVVPYGDYEAVD 359
DB 253 PPLAGTVMWMTILIVSACAPWMSKTGGLGVDAGSLPALARGHRVMTVAHPYGNVAEAD 312
QY 360 VGVAKYKKAAGODMEVNYFPAVYIDGVDVFEIDAPLPRHROEDYIGSSROEIMKMLFCK 419
DB 313 IGVAKRYKVAAGODEVYTFHTYIDGVDIVFIDSPFRNLESNTYGGNRDLILRRMVLFCCK 372
QY 420 AAVEVPMHVPCGVVPYGDNLVFLANDMTALLPYTLKAYRRHGLMOTRSLMVIHNA 479
DB 373 AAVEVPMHVPCGGICYGDNLVFLANDMTALLPYTLKAYRRHGLMOTRSLMVIHNA 432
QY 480 HOGGRPVDEPFTELPHYLEHFEFLYDPVGEHANVFAALIKRADOVVVSPGYLWELKT 539
DB 433 HOGGRPVDEPNVYDLSGNVYDLPRKVPDVGHEHNFIAALKLRADRLVYVSHQYAMELKT 492
QY 540 VEGVGGLHDIIRQNDKTRGIVNGIDMKNWNPVVDVHLKSDGTNTSLGLTDSGKQCKE 599
DB 493 SEGGMGLHNIINESDMKFRGIVNGVDTKMNPQFDALTSIDGTNTNKLQTKGKQCKA 552
QY 600 ALQRELGIOYRADVPLIGFTIGRLDGQKVEIILADAMPVIVSODVOLVMLGTGSHDESLM 659
DB 553 ALQRELGIPVREDVPIISFTIGRLDHQGVLLIAEAIWMMSHVQVLMCTGADLEQWL 612
QY 660 RHFERREHDKVAVGVSVLARRITAGADALLMPSFPECGINQLYAMAYGVTVPVYHAY 719
DB 613 KEFEAQHCDKTRSWGVSVKMAHRTITAGSDILLMPSRFEECGINQLYAMSGTVPVYHGV 672
QY 720 GGVDVTPPDPENHSGIGWTEDRAEAKLIEALGCLRTYRDKESMRGLOERGSODF 779
DB 673 GGLNDVQPPENPESBGVGTFFDAEANKMLAALLMNCLLIYKQYKESMEGIQERGSODL 732
QY 780 SMEBAAKLYEDVLLKAKYQW 799
DB 733 SMDNAAQYEEVLLVAAKQYQW 752

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RP SEQUENCE FROM N.A., AND SEQUENCE OF 66-75.
RC STRAIN=cy. Desiree; TISSUE= tuber;
EX MEDLINE=95400340; Pubmed=7670507;
RA Edwards A., Marshall J., Sidedottom C., Vissers R.G.F., Smith A.M.,
RA Martin C.;
RT "Biochemical and molecular characterization of a novel starch
RT synthase from potato tubers.";
RL Plant J. 8:283-294(1995).
CC -1- FUNCTION: ACCOUNTS FOR ONLY 10 TO 15% OF THE TOTAL SOLUBLE STARCH
CC SYNTHASE ACTIVITY IN TUBERS.
CC -1- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl) (N) =
CC UDP + ((1,4)-alpha-D-glucosyl) (N+1).
CC -1- PATHWAY: Starch biosynthesis.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST/AMYOPLAST, SOLUBLE AND GRANULE-
CC BOUND.
CC -1- SIMILARITY: Belongs to the glycoseyltransferase family 1.
CC Bacterial/plant glycogen synthase subfamily.
CC -----
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CC or send an email to license@1eb-sib.ch).
CC -----
CC EMBL: X87988; CA61241.1; -.
CC PIR: T07667; T07667.
CC InterPro: IPR001296; Glyco.trans.1.
CC Pfam: PF00534; Glycos.transf.1; 1.
CC Glycogen biosynthesis; Transferase; Glycosyltransferase;
CC Transf. peptide; Chloroplast; Amyloplast; Starch biosynthesis.
CC NON_TER 1
CC TRANSIT 1
CC CHAIN 66
CC BINDING 310
CC VARIANT 71
CC SEQUENCE 788 AA; 87890 MW; 8D8B90611E862B7B CRC64;

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Query Match 47.4%; Score 2028.5; DB 1; Length 788;  
Best Local Similarity 52.4%; Pred. No. 1.9e-105; Indels 65; Gaps 12;  
Matches 406; Conservative 107; Mismatch 197;

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QY 45 WPPQR---TARDGVAAPAAKQDAKYDDAASAPQPRARGAATVAREBDVKTLDR 101
DB 59 WRNGVKAATGNSGGAABADESNDL-LQVTLKSKKYLAMQODLLOQIAERKAVVSSIKS 117
QY 102 DAA-----EGGAPL-----PPAPRQDAARPPMNKGT.PVNGENKSTGGGATDSGLPA 149
DB 118 SLANAKGTVDGSGSLSDVDIPVDVKDYNVTVPSTAAITGIDVDKNT----- 164
QY 150 PAPAHPSTQNEVPVNGENKANAASPTSLAEVVA.PSAATISIDRAPEVPAEKPP 209
DB 165 PPAISHDVESKREIK-RDLADERAPLSRSISLN-SQISSTYSKRTLN-VPEPFPKS 221
QY 210 SSGSNFVVASAPRLDID---SDVEPLKKGAVIVEAPAPKALSPAAAVQEDLMDF 265
DB 222 SQETLLDVNSKSLVDVPGKKIQSYMPSLRKSSASHTVEQNNENLEGSASAPNEET--- 277
QY 266 KYIIGFEEFVEAKDDGMAVADAGSFEHQNHDSGFLAGENNVNVVVAACSPWCKTG 325
DB 278 -----EDPVNI-----DEKPPPLAGTVMWMTILIVSACAPWMSKTG 313
QY 326 LQDVAGALPKALAKGHRVWVVPYGDYEBAIVGVKRYTKAAGODMEVNYFPAVYIDG 385
DB 314 LQDVAGALPKALARGHGVWVVAAPRYDNPPEPDSGVKIKIKYVDGQDVVDVYTFALLMDC 373
QY 386 DVEFIDAPLPRHROEDYIGSSROEIMKMLIFCKAAVAVPMHVPCGVVPYGDNLVFLAN 445
DB 374 DVEFISHMFRILGNITIGKRVNVLKMKVLFCKAIVPMHVPCGVVPYGDNLVFLAN 433
QY 446 DWHTALLPYTLKAYRRHGLMOTRSLMVIHNAHQGVPDEPFTELPHYLEHFEFLY 505

```

Db 434 DWTALLPAYLKAYYRDNQINXMYTRSVLVHNIAHQSGPLEDFSVDLPHYMDPFLY 493  
 Qy 506 DVGGEHNNYFAAGKMDQVVVVPGYIMELKXTEGGMGLHDIIRONDWTRGVNGID 565  
 Db 494 DVGGEHNNYFAAGKMDQVVVVPGYIMELKXTEGGMGLHDIIRONDWTRGVNGID 553  
 Qy 566 NNEWNPVDVHL-KSDGYTNFSLGLTDSGKROCKEALQRELGQYRADVPLGLFGRLDG 624  
 Db 554 TKEMNPDLVHLPRSDGYNNYSILDITQTKPOCKAALQKEKGLPYRDDVPLGLFGRLDP 613  
 Qy 625 QKGVEILADAMPNYSQDVQVLMGLGRDLDSMLRHFEREHNDKRWNGSVPLARI 684  
 Db 614 QKGVDLIAEAVPMWGDVQVLMGLGRDLDSMLRHFEREHNDKRWNGSVPLARI 673  
 Qy 685 TAGADALMPSRPEPCGALNOLYAMAYGTVPVVHAGVADTVPPDPFNHSGLGWTFDRA 744  
 Db 674 TAGADILMPSRPEPCGALNOLYAMAYGTVPVVHAGVADTVPPDPFNHSGLGWTFDRA 733  
 Qy 745 EAHKLEALGHCITRTYDYKESWRGLQERGNQDPSMEHACLIEDYLAKAYQW 799  
 Db 734 EASQILPIRNCLITRYEKKSWEGLQTRCMTQDLSMDNAQNYEVLIAKAYQW 788

## RESULT 3

UGS2\_SOLUTU STANDARD; PRT; 641 AA.

AC P93568;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Soluble glycogen (starch) synthase, chloroplast precursor  
 (EC 2.4.1.11) (SS 1).  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamiales; Solanales; Solanaceae; Solanum.  
 NCBI\_TaxID=4113;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Desiree; TISSUE=leaf;  
 RA MEDLINE=97164391; PubMed=9011082;  
 RX Abel G.U.W., Springer F., Willmitzer L., Kosmann J.;  
 RT "Cloning and functional analysis of a cDNA encoding a novel 139 kDa  
 starch synthase from potato [Solanum tuberosum L.]";  
 RL Plant J. 10:981-991 (1996).  
 CC -|- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =  
 UDP + {(1,4)-alpha-D-glucosyl}(N+1).  
 CC -|- PATHWAY: Starch biosynthesis.  
 CC -|- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST. SOLUBLE (BY  
 SIMILARITY).  
 CC -|- SIMILARITY: Belongs to the glycosyltransferase family 1.  
 CC Bacterial/plant glycogen synthase subfamily 1.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 DR EMBL: Y10416; CAA71442.1; -.  
 DR PIR: T07668; T07668.  
 DR InterPro: IPR001296; Glyco\_transf\_1.  
 DR Pfam: PF00534; Glycos\_transf\_1.  
 KM Glycogen biosynthesis; Transferase; Glycosyltransferase;  
 FT Transit peptide; Chloroplast; Amyloplast; Starch biosynthesis.  
 FT TRANSIT 1  
 FT CHAIN ? 641 CHLOROPLAST (POTENTIAL).  
 FT BINDING 145 145 UDP-GLUCOSE (BY SIMILARITY).  
 SQ SEQUENCE 641 AA; 70608 MW; 30F8B0546CEB74C CRC64;

Query Match 27.5%; Score 1176; DB 1; Length 641;

Best Local Similarity 45.2%; Pred. No. 3,1e-58;  
 Matches 250; Conservative 72; Mismatches 181; Indels 50; Gaps 12;  
 Qy 263 AVADDDAGSFEHNC--NHDGSLAGEN-----VMVVVVAACSPMCKTGGLGDA 330  
 Db 94 SVAGDATTMESHSIIVANDRDLSEDEEMBEPIKLTFTIITVTAABAYSTGGLGDC 153  
 Qy 331 GALPKLAKGHRVNVVPRY-----GDYEAVDVGRKYYKAAQDMENVYFAYTD 383  
 Db 154 GSLPMLAARGHRVNVVSPRYLNGGSPDEKYNANVLDVRAVHCFGDAQEVAFYHEYRA 213  
 Qy 384 GDFVFIDALFRH---RQEDING--GSRQIKKMLPCKAAVEPMHVPGGGVYGG 438  
 Db 214 GDMVPEVDHSSYCRPGTPIGDIAGFDNQ--FRFTLSHAACEAPLVPLGSGFTYGE 269  
 Qy 439 NLVEIANDWHTALLPYLKAYYRDHGLMOYTESIMVHNIAHQSGRPVDFEFTLPEHY 498  
 Db 270 KCLFLANDWHTALLPYLKAYYRDHGLMOYTESIMVHNIAHQSGRPVATYNNLGLPPQW 329  
 Qy 499 LEHRLYDVP-----GGEHANNYFAAGKMDQVVVVPGYIMELKXTEGGMGLHDI 550  
 Db 330 YGAVEWIETPWABAHALDTGETVNVKGAIAVADRILTVSQYSWEITTPEGGYGLHEL 389  
 Qy 551 RQNDWKTGIVNGIDNMENPEVDVHLKSDGYTNFSLGLTDSGKROCKEALQRELGQVR 610  
 Db 390 SSRQSVANGITNGIDVNDMNPSTDEHIAQ---HYSINDL-SGKYQCKTDLQKELGLPR 444  
 Qy 611 ADVPILGFIIRGLDQKVEILADAMPNYSQDVQVLMGLGRDLDSMLRHFEREHNDK 670  
 Db 445 PDCLFIFIRRLYQKXVDIILSAIPELMQNTQVVMGLSGEKQYDWMKHTNLPRDKF 504  
 Qy 671 RGVWGSVRLAHRITAGADALMPSRPEPCGALNOLYAMAYGTVPVVHAGVADTVPPD 730  
 Db 505 RAWGVNVPVSHRITAGCDILMPSRPEPCGALNOLYAMAYGTVPIHSTGLADTYKDFN 564  
 Qy 731 PFNHSGL-----GWTFDRAEAKHLEALGHCITRTYDYKESWRGLQERGNQDPSMEHAAK 786  
 Db 565 PYAQEGIGEGTGWTFSELTSEKLDITKLAIGYTEHKSWEGLMRGMGRDYSWENAAI 624  
 Qy 787 LYEDVLLAKAYQW 799  
 Db 625 QYEGV-----FTW 632

## RESULT 4

UGS2\_ARATH STANDARD; PRT; 652 AA.

AC Q9RNE2; Q9RNE2;  
 DT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Soluble glycogen (starch) synthase, chloroplast precursor  
 (EC 2.4.1.11) (SSS).  
 GN AT5G24300 OR MOP9.12.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eustoidae II; Brassicales; Brassicaceae; Arabidopsi.

CC NCB1\_TaxID=3702;  
 [1]  
 RP SEQUENCE OF 78-652 FROM N.A.  
 RA Lue W.L., Wang S.M., Yu T.S., Chen J.;  
 RT "Characterization of Arabidopsis soluble starch synthase gene";  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

CC -----  
 CC This entry is a structural analysis of Arabidopsis thaliana chromosome 5. II.  
 CC Sequence features of the regions of 1,044,062 bp covered by thirteen  
 CC physically assigned P1 clones.;



RL DNA Res. 4:291-300(1997).  
 RN [3]  
 RC SEQUENCE FROM N.A.  
 RP STRAIN=cy. Columbia;  
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.,  
 RT "RISKEN Arabidopsis full length cDNA clones (RAPFs) sequenced by the  
 RL SSP consortium (Salik/Stanford/PGSC)."  
 CC Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl) (N) =  
 CC UDP + ((1,4)-alpha-D-glucosyl) (N+1).  
 CC -1- PATHWAY: Starch biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: Amyloplast or chloroplast, soluble (By  
 CC similarity).  
 CC -1- SIMILARITY: Belongs to the glycosyltransferase family 1.  
 CC Bacterial/plant glycosyltransferase subfamily.  
 CC -----  
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 CC -----  
 CC EMBL: AF121673; AAF24126.1; -  
 CC EMBL: AB06701; BAB10396.1; -  
 CC EMBL: AY128273; AAM91082.1; -  
 CC InterPro: IPR001296; Glyco\_transf\_1.  
 CC Pfam: PF00534; Glycos\_transf\_1.  
 CC Glycosyltransferase; Glycosyltransferase;  
 CC Transf. peptidase; Chloroplast; Amyloplast; Starch biosynthesis.  
 CC TRANSIT ? ? ?  
 CC CHAIN ? ? ?  
 CC BINDING 156 156 85  
 CC CONFLICT 78 85  
 CC CONFLICT 89 89  
 CC CONFLICT 222 222  
 CC CONFLICT 584 584  
 CC SEQUENCE 652 AA; 72098 MW; 91E5069DCD1B2B58 CRC64;  
 Query Match 27.5%; Score 1175.5; DB 1; Length 652;  
 Best Local Similarity 42.2%; Pred. No. 3.4e-58;  
 Matches 248; Conservative 83; Mismatches 179; Indels 77; Gaps 13;  
 QY 269 IGFEFVEAKDDGMAYADAGSFEHQNH-----DSGLA 303  
 DB 78 LGFQ--LTPPGDQCTSTSTGEITHEEKEKALDQVADFGVGNRAVERGALEVGIPS 135  
 QY 304 G--ENNVNVVVAALGSPCKTGGIADVAGALPKLAKRGHVVVVVRY-----GDY 354  
 DB 136 GRAEVNNVNVFTVSEAPYSKTGIGADVCGSLPILAGRGHVVWISRYLNGTADAKY 195  
 QY 355 EEAIVGVKRYKAAQDMENVVPHAYIDGVDFVTDAPLFRHQEDIIYGSR--QETM 411  
 DB 196 ARAKIDGIRVTVNCFGSGQEVGFYHEDYRDGVDMVFVDHKSX-HRGNPFQDSKGAFGNQ 254  
 QY 412 KEMILFEKAAVEPVMHVPDGGVPGVPGDGNVETANDMHTALLPVYLKAYRPHGIMQYRS 471  
 DB 255 FRTLLCHAAACEPLVPLGSGFTYGKSL-FLVNDMHAAGVETLLAAKRPYGVYKDKAS 313  
 QY 472 IWINHIAHQGRPVDFEFTTELPEHYLHFRLYDPVG-----GEHANYFA 517  
 DB 314 ILIHNLAAQGVAPATYTNLGLPSEM-----YAGVGVVPTMARATLDDGEAVNYLK 367  
 QY 518 AGLKADQVVVSPGLMELKTVGSGMGLHDIIRQDMKTRGIVNGIMMENPEVDHL 577  
 DB 368 GALTVDRIITVSGRAMETTVGSGYGLDLSRSKSVYINGIINGINDEMPSTDEHI 427  
 QY 578 KSDGYTNFSLGLTD-SGRQCKEALQRELGLQVRADVPVLGFIIGLDGQKVEIADAMP 636  
 DB 428 P-----FHYSDADVESEKIKCMAKQELGLPIRPECPIGFIIGRLDYKGIDLIQTGF-481  
 QY 637 WIVSGDVGLVMTGTGSHDLESMLRHERRHHDKVRGWFVRLAHRTIAGDALMLMSR 696

DB 482 DLMVDDIQFVNLGSDPKYSEWMSMETTYRDKRGWGVFVPISHRTAGCDLILMSR 541  
 QY 697 FEPGGLNQLYAMAAGTVFVAVAGVDRDTPFPDFENH-----SGLGWTFDRAAHKLEA 752  
 DB 542 FEPGGLNQLYAMARVETIIVVAGTGLRDTVENPENVAGAGAGTGNWFTLSKDSMWSA 601  
 QY 753 LGHCRTTRDYKESRRCIGERMSQDSEWEHAKLYEVLAKKQW 799  
 DB 602 LRLAAATVEYKQSGWEGMLRGMRTNYSWENAAVQYEV-----FQW 643  
 RESULT 5  
 UGS2 WHEAT  
 ID UGS2 WHEAT STANDARD; PRT; 610 AA.  
 AC Q43654;  
 DT 01-NOV-1997 (rel. 35, Created)  
 DT 01-NOV-1997 (rel. 35, Last sequence update)  
 DT 15-SEP-2003 (rel. 42, Last annotation update)  
 DE Soluble glycosyl (starch) synthase, chloroplast precursor  
 DE (EC 2.4.1.11) (Fragment).  
 OS Triticum aestivum (wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticaceae; Triticum.  
 OX NCBI\_TaxID=4565;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cy. T.A. Florida; Tissue=Endosperm;  
 RA Block M., Loerz H., Juetzke S.;  
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl) (N) =  
 CC UDP + ((1,4)-alpha-D-glucosyl) (N+1).  
 CC -1- PATHWAY: Starch biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST, SOLUBLE (BY  
 CC SIMILARITY).  
 CC -1- SIMILARITY: Belongs to the glycosyltransferase family 1.  
 CC Bacterial/plant glycosyltransferase subfamily.  
 CC -----  
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 CC -----  
 CC EMBL: U48227; AAB02197.1; -  
 CC DR PIR: T06280; T06280.  
 DR InterPro: IPR001296; Glyco\_transf\_1.  
 DR Pfam: PF00534; Glycos\_transf\_1.  
 CC Glycosyltransferase; Glycosyltransferase;  
 CC Transf. peptidase; Chloroplast; Amyloplast; Starch biosynthesis.  
 CC TRANSIT ? ? ?  
 CC CHAIN ? ? ?  
 CC BINDING 7 7  
 CC SEQUENCE 610 AA; 67143 MW; 46080A3B7B87193 CRC64;  
 Query Match 26.4%; Score 1127.5; DB 1; Length 610;  
 Best Local Similarity 48.1%; Pred. No. 1.4e-55;  
 Matches 235; Conservative 69; Mismatches 158; Indels 27; Gaps 9;  
 QY 316 EGSFPCKTGGIADVAGALPKLAKRGHVVVVPRY-----GDYEAIVGVKRYK--AA 369  
 DB 1 EAPYAKSGSLGADVCGSLPILAGRGHVVWVPRYLNSSPXNKAALYTKHIKIPCF 60  
 QY 370 GDMENVVPHAYIDGVDFVTDAPLFRHQEDIIYGSR--QETM 426  
 DB 61 GGSHEVTFPEYEDNDVWFVHDPSY-HRPGSLYGNFAGFGNCRVTLCTAACAEVL 119  
 QY 427 HVCQGVYDGNLVETIANDMHTALLPVYLKAYRPHGIMQYRSIWINHIAHQGRPV 486

DB 120 ILEGGYIYGO-NCMEFVNDMHASLVLLAAKRPYGVYRDSRSTLVINHIAHGVBEPA 178  
QY 487 DEEPFTLPEHYL-----EHRFLYDPVGEHANVFAAGLGMADQVWVSPGYMEK 538  
DB 179 STYDGLPEPEWGALEWTPPEWARRALDKGANVFLKAAVTAARIVTSSGYMEWT 238  
QY 539 TWEGGWLHDIIRONDKRTGIVNGIDNMENPEVDVHLKSDYTNFSLGTLDSGRCK 598  
DB 239 TAEGGGLNELLSRSKSVLNGIIVNGIDINDMPTDKLPH---HYVVDL-SGAKCK 293  
QY 599 EALOREGLQVRAVPLIFGTRLDGQKVEITADANPMVSDVQVUMLGTERHLESM 658  
DB 294 AELQKEGLPVREVPPLIGFGRLDYQKIDILKMALPELMREDVQFVMLGSDPIFEGM 353  
QY 659 LRHFERHDKVKGWGVFSYRLAHRITAGADALIMPSPCGINQYANAYGTVPVHA 718  
DB 354 MRSTESSYKQFRGMVGSVPVSHRITAGCDILMPSPCGINQYANAYGTVPVHA 413  
QY 719 VGVYRDTVPPEDP---NHSGLGTPRAAHKILIELGHLRTYDYESWGLQBERG 775  
DB 414 TGGRLDTVEFTNFPGAKGEEGTGWAFFSLTVDKLMLRTAMSTFRHRSWGLMKRG 473  
QY 776 SODFSMEHA 784  
DB 474 TKDHTMDHA 482

## RESULT 6

UGST\_ORYSA STANDARD; PRT; 626 AA.

AC 040739;  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Soluble glycogen [starch] synthase, chloroplast precursor  
DE (EC 2.4.1.11) (SSS).  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Eumetazoa; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Eriactolaceae; Oryzaceae; Oryza.  
NCBI TaxID=4530;

SEQUENCE FROM N.A., AND SEQUENCE OF 114-131.

RA Kobaishi E., Ohnishi S., Tanaka K.-I., Arai Y.,  
RT "Identification, cDNA cloning, and gene expression of soluble starch  
RT synthase in rice (Oryza sativa L.) immature seeds.";  
RL Plant Physiol. 103:565-573 (1993).  
CC -1- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl} (N) =  
CC UDP + {(1,4)-alpha-D-glucosyl} (N+1).  
CC -1- PATHWAY: Starch biosynthesis.  
CC -1- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST, SOLUBLE.  
CC -1- TISSUE SPECIFICITY: LEAVES AND IMMATURE SEEDS.  
CC -1- MISCELLANEOUS: THREE FORMS OF SOLUBLE STARCH SYNTHASE WERE  
CC PURIFIED: RRS1, RRS2 AND RRS3.  
CC -1- SIMILARITY: Belongs to the glycocyltransferase family 1.  
CC Bacterial/plant glycogen synthase subfamily.

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DR EMBL, D16202; BAA03739.1;  
DR F1R, J02322; J02322.  
DR Gramene; Q40739;  
DR InterPro; IPR001296; Glyco\_transf\_1.  
DR Pfam; PF00534; Glyco\_transf\_1; 1.

KW Glycogen biosynthesis; Transferase; Glycosyltransferase;  
KW Transit peptide; Chloroplast; Amyloplast; Starch biosynthesis.  
FT TRANSIT 1 113 CHLOROPLAST (POTENTIAL).  
FT CHAIN 114 626 SOLUBLE GLYCOSYL (STARCH) SYNTHASE, RRS3.  
FT CHAIN 112 626 SOLUBLE GLYCOSYL (STARCH) SYNTHASE, RRS1.  
FT BINDING 147 147 UDP-GLUCOSE (BY SIMILARITY).  
SQ SEQUENCE 626 AA; 68451 MW; 03E4182507D26658 CAC64;

Query Match 24.8%; Score 1060; DB 1; Length 626;  
Best Local Similarity 36.5%; Pred. No. 8.2e-52;  
Matches 258; Conservative 79; Mismatches 218; Indels 152; Gaps 16;

QY 58 ARAAKKARVDDDAASRQPARAGAAATVARRDPVTKLDDAEGAPAPAPAPROD 117  
DB 2 ARAAG---MGIGAACTVAPQVPRRRRLRQVRRRCVABLSHDSAGPLAPPLVK 56  
QY 118 AARPSM---NGTPVNGENKSTGGGATKDSLPAPAPAPSPQNRVNVNGENKANVAS 174  
DB 57 QPVLPFLVPTSTP-----PAPQSPAPA----- 80  
QY 175 PPTSLAEVAPDPAATISIDKAPESVPAKPPSSGNSNVVASAPRLDIDSDVEBEL 234  
DB 81 -----FTPEPLPDGCV-----GTEPDL 98  
QY 235 KKGAVIVEAPNPKALSPAPAPVQEDLMDKRYTGFEEPEVAAVDGMAVADAGSFEH 294  
DB 99 E-----GLTEDSIDKTIIFASQSEIMD---VREQA----- 127  
QY 295 QNHDSGLAGENVWVVALECSFWCTGGLGDAVAGALPQALAKGRRVAVVPRY--- 351  
DB 128 -----QAKVRSVVFVTGASAPYAKSGGLGVCGSLPILALRGHRVAVVPRYWG 179  
QY 352 ---GTYEAYDGVAKYKKAAGODWENVYFRAVIDGVFIDAPLFRHOEDIVG---G 405  
DB 180 ALNKNFANFYEKIKITPCGGEHEVTFHEHYDSUDVWVVDHPSY-HRGNLYGDVFG 238  
QY 406 SROEIMKRMILECKAAVEPMWPCGVPGYDGNLVIANDMHTALFVYLKAYRDHGL 465  
DB 239 AFGDQNFRTLLCYAACAPLILLEGYIYGO-KCMFVNDMHASLVLLAAKRPAPG 297  
QY 466 MGYTSIMVTHIAQSGPVDPEPFTLPEHYL-----EHRFLDPVGEHANVFA 517  
DB 298 YDASVVLVHNLAAQGVBPASTYDPLDLPBWYALCWVPEAKRRALDKGANVPLK 357  
QY 518 AGLKNAQDVVAVSPYLWELKTEGGMGLHDIIRONDKRTGIVNGIDNMENPEVDVHL 577  
DB 358 GAVVADRIIVTVSSQSWEVTTAEGGGLNELLSRSKSVLNGIIVNGIDINDMPTDKL 417  
QY 578 KSDGTNFTSLTLDGSKQCKEALRELGLCYRADVPLIFGTRLDGQKVEITADANPM 637  
DB 418 P-----YHYSVDL-SGAKCKRELKELGLFPRVPLIFGTRLDYQKIDILKALPD 472  
QY 638 IYSDVQVLMGTGRHDLSEMLRHFERHDKVKGWGVFSYRLAHRITAGADALIMPSP 697  
DB 473 LMRDNIQFMFGSDGDPFGEGMRSTESGYRLFRGMVGSVPVSHRITAGCDILMPSP 532  
QY 698 EPGGGLQYAAAYGVVAVGVYRDYVPEDP---NHSGLGTF 741  
DB 533 EPGGGLQYAAAYGVVAVGVYRDYVPEDP---NHSGLGTF 741

## RESULT 7

UGST\_ANTMA STANDARD; PRT; 606 AA.

AC 082627;  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Granule-bound glycogen [starch] synthase, chloroplast precursor  
DE (EC 2.4.1.11) (GBSSI).  
GN MAXY OR GBSS.  
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
CC Asteridae; lamiales; Malvales; Antirrhinaceae; Antirrhinae;  
CC Antirrhinum.  
CC NCBI\_TaxID=4151;  
CC [1]  
CC SEQUENCE FROM N.A.  
CC TISSUE=Leaf;  
CC PubMed=10364391;  
CC Merida A., Rodriguez-Galan J.M., Vincent C., Romero J.M.;  
CC "Expression of the granule-bound starch synthase I (GbsSSI) gene from  
CC RT snapdragon is developmentally and circadian clock regulated.";  
CC RT Plant Physiol. 120:401-410(1999).  
CC -1- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl)(N) =  
CC UDP + ((1,4)-alpha-D-glucosyl)(N+1).  
CC -1- PATHWAY: Starch biosynthesis.  
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.  
CC -1- TISSUE SPECIFICITY: In leaves, flowers and fruits. Observed in all  
CC floral whorls at early developmental stages, but restricted to  
CC carpel before anthesis.  
CC -1- INDUCTION: Expressed with a circadian rhythm with peak expression  
CC at the end of the day.  
CC -1- SIMILARITY: Belongs to the glycoseyltransferase family 1.  
CC Bacterial/plant glycogen synthase subfamily.  
CC -----  
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CC -----  
CC EMBL: AJ006293; CA06958.1; -  
CC DR EMBL: AJ006294; CA06959.1; -  
CC DR InterPro: IPR001296; Glyco. trans. 1.  
CC Pfam: PF00534; Glycosyl transferase; Glycosyltransferase;  
CC Glycogen biosynthesis; Transferrase; Glycosyltransferase;  
CC Transf. peptidase; Chloroplast; Starch biosynthesis;  
CC TRANSIT 1 78 CHLOROPLAST (BY SIMILARITY).  
CC CHAIN 79 608 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.  
CC BINDING 96 96 UDP-GLUCOSE (BY SIMILARITY).  
CC FT SEQUENCE 608 AA; 66361 MW; 652753D5658E0C CRC64;  
CC  
CC Query Match 22.3%; Score 954; DB 1; Length 608;  
CC Best Local Similarity 41.5%; Pred. No. 6,1e-46;  
CC Matches 218; Conservative 79; Mismatches 188; Indels 40; Gaps 13;

DB 421 ISKFEVLGVQIIILGKTKKFFEQIOLELYEDKRGVAKENVPLAMITAGADFMVLP 480  
QY 695 SREPCGGLNOLYAMAVGTVPVAVAGGVDPVPP-EDPNNHSLG---WTPRAEAKHLI 750  
DB 461 SREPCGGLNOLYAMAVGTVPVAVAGGVDPVPP-EDPNNHSLG---WTPRAEAKHLI 750  
QY 751 EALGHCRTYRD-YKESWRGLQERKSDPSEHAKLYEDVLL 793  
DB 541 TVERALAAVGSVAYKE---MIONCAODLEWKPGRKWKML 581  
RESULT 8  
ID UGST\_MANES STANDARD; PRT; 608 AA.  
AC Q43784;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Granule-bound glycogen [starch] synthase, chloroplast precursor  
DE (EC 2.4.1.11).  
DE MAXY OR GBS.  
OS Manihot esculenta (Cassava) (Manihot).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC Eucosids I; Malpighiales; Euphorbiaceae; Manihot.  
CC NCBI\_TaxID=3983;  
CC [1]  
CC SEQUENCE FROM N.A.  
CC STRAIN=cy. M. COL 22; TISSUE=tuberous root;  
CC MEDLINE=94083565; PubMed=826633;  
CC RA Salehuzzaman S.N., Jacobsen E., Visser R.G.F.;  
CC "Isolation and characterization of a cDNA encoding granule-bound  
CC RT starch synthase in cassava (Manihot esculenta Crantz) and its  
CC antisense expression in potato.";  
CC RT Plant Mol. Biol. 23:947-962(1993).  
CC -1- FUNCTION: RESPONSIBLE FOR THE SYNTHESIS OF AMYLOSE IN RESERVE  
CC STARCH.  
CC -1- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl)(N) =  
CC UDP + ((1,4)-alpha-D-glucosyl)(N+1).  
CC -1- PATHWAY: Starch biosynthesis.  
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.  
CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN A NUMBER OF DIFFERENT ORGANS,  
CC BUT MOST ABUNDANTLY IN TUBERS.  
CC -1- SIMILARITY: Belongs to the glycoseyltransferase family 1.  
CC Bacterial/plant glycogen synthase subfamily.  
CC -----  
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CC -----  
CC EMBL: X74160; CA52273.1; -  
CC DR PIR: S43341; S43341.  
CC DR InterPro: IPR001296; Glyco. trans. 1.  
CC Pfam: PF00534; Glycosyl transferase; Glycosyltransferase;  
CC Glycogen biosynthesis; Transferrase; Glycosyltransferase;  
CC Transf. peptidase; Chloroplast; Starch biosynthesis;  
CC TRANSIT 1 78 CHLOROPLAST (BY SIMILARITY).  
CC CHAIN 79 608 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.  
CC BINDING 96 96 UDP-GLUCOSE (BY SIMILARITY).  
CC FT SEQUENCE 608 AA; 66361 MW; 652753D5658E0C CRC64;  
CC  
CC Query Match 22.2%; Score 948; DB 1; Length 608;  
CC Best Local Similarity 41.5%; Pred. No. 1,3e-45;  
CC Matches 216; Conservative 77; Mismatches 172; Indels 56; Gaps 12;

QY 368 AAGQDMENVYFHAAYIDGVDFVFIADPLFRHROEDIVG--GSR-----QELMKMI 415  
 DB 142 IGDRIETVRFPHSYKRGVDRVFDHPMF---LEKVMGKTSKITYGPRAGLDYDNDQIRFS 198  
 QY 416 LFCKAAVEVPMHVCQGV-----PYGDNVFIANDMHTALLPVYLKAYYRDHGLMOYTR 470  
 DB 199 LLLCAALBAPRVNLNSSKQFSGPYGE-EVAFIANDMHTALLPVYLKAYYRDHGLMOYTR 257  
 QY 471 SIMVTHINIAHQGRPVDEFPTLPEHYLHEHFLYD---PVGSHANYFAAGLKMAQOV 526  
 DB 258 VAFCHINIAVQGRFAFSDPFLNLPDKFKSSPFDIDGKPKYKGRKIMMKAGILSDRY 317  
 QY 527 VVVSPEGYLME-LKTYEGGNGLHDIIRQNDMKTGIVNGIDMNMENPEVDVHLKSDGYTF 585  
 DB 318 LTVSPYVAQEVISGVERGVDELNFTKRG--IAGIINGMDVQWNPVTDKTID---IHX 371  
 QY 586 SLGTLDSGRQCKEALQRELGLQVADVPYLLGFIRLDGQGVYIADAMPWISQDYL 645  
 DB 372 DATVMDAKPPLKELALQAEVGLPVDRNVPILGIFGRLEBQKSDIPVAALISQVHNVOI 431  
 QY 646 VMLGTGRDLLESLMRFERHNDKRGWVGSVRLAHRITAGADALLMPSRFGCINOL 705  
 DB 432 VILGKKKFKFEKQJLEHLEVLVPDKARGVAKFNVPALHNTITAGADFMLVPSRFGCINOL 491  
 QY 706 YANAVGTVPVNAVGVADVPDPDPFNHSGLGWT-----FDRBAHKLIEA 752  
 DB 492 HAMRGVTPVASTGGLVDIVKE-----GYTGQMGALHYECOKIDQADVAALVKT 542  
 QY 753 LGHCRTYRDYKESKRGLOERGMQSDPSWEHAALKYEDVLL 793  
 DB 543 VARALGTVA--TAALREMLINCMADLSMKGPARKWEXKLL 581

## RESULT 9

USGT\_IPQBA STANDARD; PRT; 608 AA.  
 ID USGT\_IPQBA  
 AC 042857;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Granule-bound glycogen [starch] synthase, chloroplast precursor  
 (EC 2.4.1.11).  
 GN WAXY OR S657.  
 OS Ipomoea batatas (Sweet potato) (Batate).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamiales; Solanales; Convolvulaceae; Ipomoeae.  
 OX NCBI\_TaxID=4120;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Tainong 57; TISSUE=tuberous root;  
 RA Wang S.-J., Yeh K.W., Tsai C.Y.;  
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: REQUIRED FOR THE SYNTHESIS OF AMYLOSE IN ENDOSPERM.  
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl} (N) =  
 CC UDP + {(1,4)-alpha-D-glucosyl} (N+1).  
 CC -1- PATHWAY: Starch biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND (BY SIMILARITY).  
 CC -1- SIMILARITY: Belongs to the glycosyltransferase family 1.  
 CC Bacterial/plant glycogen synthase subfamily.  
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 CC EMBL: U44126; AAA86423.1; -  
 DR PIR: T10906; T10906  
 DR InterPro: IPR001286; GlycoTrans 1.  
 DR Pfam: PF00354; Glycos\_Transf\_1; I.

KW Glycogen biosynthesis; Transferase; Glycosyltransferase;  
 KW Transit peptide; Chloroplast; Starch biosynthesis;  
 FT TRANSIT 1 76 CHLOROPLAST (BY SIMILARITY).  
 FT CHAIN 77 608 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.  
 FT BINDING 96 96 UDP-GLUCOSE (BY SIMILARITY).  
 SQ SEQUENCE 608 AA; 67000 MW; CCA8FA50A2F69CB0 CRC64;

Query Match 21.3%; Score 910; DB 1; Length 608;  
 Best Local Similarity 41.8%; Pred. No. 1.7e-43;  
 Matches 214; Conservative 70; Mismatches 190; Indels 38; Gaps 11;

QY 308 MNVNVVAAECSPWCKTGIGLGVAGALPRALAKGRHVVVVVRYGYDEAYDGVKRYK 367  
 DB 82 MNLVTVGCEBGPCKTGIGLGVAGLPPALARGHVVTVGCRDYQYDAMETCVVVEPQ 141  
 QY 368 AAGQDMENVYFHAAYIDGVDFVFIADPLFRHROEDIVG--GSR-----QELMKMI 415  
 DB 142 VGDRIEPAFFHSYKRGVDRVFDHPMF---LEKVMGKTSKITYGPRAGLDYDNDQIRFS 198  
 QY 416 LFCKAAVEVPMHVCQGV-----PYGDNVFIANDMHTALLPVYLKAYYRDHGLMOYTR 470  
 DB 199 LLLCAALBAPRVNLNSSKQFSGPYGE-DVAFVANDMHTALLPVYLKAYYRDHGLMOYTR 257  
 QY 471 SIMVTHINIAHQGRPVDEFPTLPEHYLHEHFLYD---PVGSHANYFAAGLKMAQOV 526  
 DB 258 VAFCHINIAVQGRFAFSDPFLNLPDKFKSSPFDIDGKPKYKGRKIMMKAGILSDRY 317  
 QY 527 VVVSPEGYLME-LKTYEGGNGLHDIIRQNDMKTGIVNGIDMNMENPEVDVHLKSDGYTF 585  
 DB 318 LTVSPYVAQEVISGVERGVDELNFTKRG--IAGIINGMDVQWNPVTDKTID---IHX 371  
 QY 586 SLGTLDSGRQCKEALQRELGLQVADVPYLLGFIRLDGQGVYIADAMPWISQDYL 645  
 DB 372 DATVMDAKPPLKELALQAEVGLPVDRNVPILGIFGRLEBQKSDIPVAALISQVHNVOI 431  
 QY 646 VMLGTGRDLLESLMRFERHNDKRGWVGSVRLAHRITAGADALLMPSRFGCINOL 705  
 DB 432 VILGKKKFKFEKQJLEHLEVLVPDKARGVAKFNVPALHNTITAGADFMLVPSRFGCINOL 491  
 QY 706 YANAVGTVPVNAVGVADVPDPDPFNHSGL-----GWTEDBAHKLIEALGHCRTYR 761  
 DB 492 HAMRGVTPVASTGGLVDIVKEGYTGFMGAFNVDCETVDEVDILKVTYGRALAIYG 551  
 QY 762 DYKESKRGLOERGMQSDPSWEHAALKYEDVLL 793  
 DB 552 TL--AFTEMIKMCKMSQELSMKGPARKWEXKLL 581

## RESULT 10

USGT\_ARATH STANDARD; PRT; 610 AA.  
 ID USGT\_ARATH  
 AC Q2MAQO;  
 DT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Granule-bound glycogen [starch] synthase, chloroplast precursor  
 (EC 2.4.1.11).  
 GN WAXY OR ATIG32900 OR F9L1.8.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eusteroideae II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Theologis A., Becker U.R., Palm C.J., Federspiel N.A., Kaul S.,  
 RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,  
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
 RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 Kim C.J., Koo H.L., Kremetskaya I., Kurts D.B., Kwan A., Lam B.,  
 Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 Lin X., Liu S.X., Liu Z.A., Lurcs J.S., Maiti R., Marzalli A.,  
 Miltcher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
 Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 Sun H., Tallon L.J., Tambunga G., Tortini M.J., Town C.D., Walker M.,  
 Utechtack T., Van Aken S., Vaysberg M., Vayotskaya V.S., Walker M.,  
 Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,  
 "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
 thaliana";  
 RA Nature 408:816-820(2000).  
 RU  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;  
 RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the  
 RT SSP consortium (Salk/Stanford/PGSC).";  
 RU Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
 RA Feldmann K.;  
 RT "Full-length cDNA from Arabidopsis thaliana";  
 RT Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: Required for the synthesis of amylose in endosperm (By  
 similarity).  
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl) (N) =  
 CC UDP + ((1,4)-alpha-D-glucosyl) (N+1).  
 CC -1- PATHWAY: Starch biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: Chloroplast, granule-bound (By similarity).  
 CC -1- SIMILARITY: Belongs to the glycyltransferase family 1.  
 CC Bacterial/plant glycogen synthase subfamily.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; AC006424; AAF3273.1; --  
 DR EMBL; AY094405; AAM19783.1; --  
 DR EMBL; AY123983; AAM74496.1; --  
 DR EMBL; AY149948; AAM31102.1; --  
 DR EMBL; AY088544; AAM6076.1; --  
 DR PIR; F86453; F86453.  
 DR InterPro; IPR001286; Glyco trans 1.  
 DR Pfam; PF00534; Glycosyltransf 1.  
 KW Glycogen biosynthesis; transferase; Glycosyltransferase;  
 KW Transit peptide; Chloroplast; Starch biosynthesis;  
 FT TRANSIT 1 80 CHLOROPLAST (BY SIMILARITY).  
 FT CHAIN 81 610 GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE.  
 FT FT BINDING 98 98 UDP-GLUCOSE (BY SIMILARITY).  
 SQ SEQUENCE 610 AA; 66879 MW; CFI1F25BE12220DF CRC64;  
 Query Match 21.2%; Score 908; DB 1; Length 610;  
 Best Local Similarity 39.2%; Freq. No. 2.2e-43;  
 Matches 223; Conservative 80; Mismatches 209; Indels 42; Gaps 12;  
 QY 273 EPEAADDGNAVDADSGFEHQNHDGFLAGENVVAVVAAEGSPWCKTGGLDVGVA 332  
 DB 59 KPVSAK-----SKRSKSKYKAKIVCEKMSVIFIGAVGPMKCTGGLDVG 108  
 QY 333 LPEALAKGRHVVVPRVDYEADVDGVRKTKYKAAGDMENVTHAYIDVDVFD 392  
 DB 109 LPALALARGHVVTCIRYDQYADVDTCVVAQIKVGDVENVRFHCYKRGVDVDF 168  
 QY 393 PLFRHR-----QEDYGG-----SRCEIMKMIIFCAAVEVPHVFCGV-----PYGDG 438  
 DB 169 PILALAVVGTGKITGPIGVVYNDQARFSLCQALAEAPVNLNSKXVFSFGYGB- 227

QY 439 NLVFANDWHTALLPVYIKAYRRDHGIMQVYASIMVTHINIAHOGRGVDEPFTEPEHY 498  
 DB 228 DVVFANDWHTALLPVYIKAYRRDHGIMQVYASIMVTHINIAHOGRGVDEPFTEPEHY 287  
 QY 499 LEHFLYD-----PYGGEHANYFAAGLKXADQVWVVSQYWEI-KTYEGGGLHDIIRON 553  
 DB 288 KSSFDMDGYEKVPYGRKINMKKALLIHAHVLTVPYPAQELISGDVGLHKKYLRMK 347  
 QY 554 DKRTGYINGIDNMENNEPVVHLKSDQYTNPSLCTDSCGRCKEALQRELGQVADY 613  
 DB 348 --TVSGIINGMDVQSWNPSTQYD---IKYDITVDAPLIREALQAAVGLPDRDV 401  
 QY 614 PLGFIIGRLDGQGVETIADAMPVIVSODVQVLMVIGRHDLESMLRFREREHNDKRGW 673  
 DB 402 PVIGFIIGRLDGQGVETIADAMPVIVSODVQVLMVIGRHDLESMLRFREREHNDKRGW 461  
 QY 674 VGFSTLHARITAGADALLMSRPFPCGLNQLYMAVGTVPYVAVGVRTVPE-FDPF 732  
 DB 462 AKENVPLAMITAGADFTIVSRFPFGLIQLHARVGTVPYVAVGTGLVTVKDXGYGF 521  
 QY 733 NMSGVWTFDRAHKLIEALGHCLRTYRDYKESWRGLQE---RGSODFSEHNAKLYE 789  
 DB 522 HIGRPVWKEVVDPPDVATKAVYRAVAVIGTS--AMQEVVKNOMDQDFWKGPARLME 579  
 QY 790 DVL 793  
 DB 580 KYLL 583  
 RESULT 11  
 ID UGST\_PEA STANDARD; PRT; 603 AA.  
 AC Q43092;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Granule-bound glycogen [starch] synthase, chloroplast precursor  
 DE (EC 2.4.1.11) (G88S1).  
 OS Pisum sativum (Garden pea).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosida 1; Fabales; Fabaceae; Papilionaceae; Viciae; Pisum.  
 CX NCBI\_TaxID=3888;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 76-88.  
 RC STRAIN=cv. BCI/RR; TISSUE=Embryo;  
 RX MEDLINE=33251108; PubMed=1302049;  
 RA Dry I., Smith A., Edwards A., Bhattacharya B., Dunn P., Martin C.;  
 RT "Characterization of cDNAs encoding two isoforms of granule-bound  
 RT starch synthase which show differential expression in developing  
 RT storage organs of pea and potato";  
 RL Plant J. 2:193-202(1992).  
 CC -1- FUNCTION: MAY BE RESPONSIBLE FOR THE SYNTHESIS OF AMYLOSE.  
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl) (N) =  
 CC UDP + ((1,4)-alpha-D-glucosyl) (N+1).  
 CC -1- PATHWAY: Starch biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN FOLDS AND LEAVES. NO EXPRESSION  
 CC IN FLOWERS OR STIPULES.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT ALL STAGES OF EMBRYONIC  
 CC DEVELOPMENT WITH HIGHEST LEVELS IN LATER DEVELOPMENTAL STAGES.  
 CC -1- SIMILARITY: Belongs to the glycyltransferase family 1.  
 CC Bacterial/plant glycogen synthase subfamily.  
 CC  
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 CC

DR EMBL: X88789; CAA61268.1; -  
 DR PIR: S61504; S61504.  
 DR InterPro: IPR001286; Glyco\_transf.1.  
 DR Pfam: PF00394; Glycosyltransferase; Glycosyltransferase;  
 KM Glycogen biosynthesis; transferase; Glycosyltransferase;  
 FT TRANSIT 1 75 CHLOROPLAST.  
 FT CHAIN 76 603 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.  
 FT BINDING 91 91 UDP-GLUCOSE (BY SIMILARITY).  
 SQ SEQUENCE 603 AA; 66362 MW; 817252PDD12CCAA0 CRC64;

Query Match 21.1%; Score 903; D8 1; Length 603;  
 Best Local Similarity 39.8%; Pred. No. 4.1e-43;  
 Matches 206; Conservative 84; Mismatches 179; Indels 48; Gaps 12;

QY 308 MNVYVVAECSPWCKTGLGADVAGALPKALAKGHEWVWVPRYGDYEAADVGRKYYK 367  
 DB 77 MSIVPGAEVGPMSKGTGLADVGLGPRYLAKGHEWVWVPRYDYKDAWDTNLVEYK 136  
 QY 368 AAGDMEVNYFAHYIDGVDFVFDAPLFRHROEDIVG-GSR-----QETWKMT 415  
 DB 137 VGDKIETVRFHCKGKGVDFVDFHDLFLER---VWGKTGSKLYGPKTGDYRDQLRFS 193  
 QY 416 LFCRAAVEVPMHVPCCGV-----PYDGNLVFIANDMHTALPVLKAYRDHGLMOYTR 470  
 DB 194 LFCRAAVEVPMHVPCCGV-----PYDGNLVFIANDMHTALPVLKAYRDHGLMOYTR 470  
 QY 471 SIMVHNIAHQGRGVDFEFPTELPEHYLEHFRLYD---PVGGEHANYFAAGLKMADQV 526  
 DB 253 VAFCHINIAVQGRNATFDFGLNLPDEFRRSFDPIGVNKKPCGKKINMKWAGILESDQV 312  
 QY 527 VVSPGYLMEKLVKVEG-GMGLHDIIRQNDKMTGTYNGIDNMENNEVVDVHLKSDGYTF 585  
 DB 313 FTVSPGYLMEKLVKVEG-GMGLHDIIRQNDKMTGTYNGIDNMENNEVVDVHLKSDGYTF 585  
 QY 586 SLGLTDSGKQCKEALQRELGQVADVPPLGFIGRLDGQKVEIITADAMPWISQDYOL 645  
 DB 367 NETTVPAKRLKGLTQAEIGLPVDSIPILGFIGRLDGQKVEIITADAMPWISQDYOL 645  
 QY 646 VMLGTGCHDLESMLRHEREHNDKRGWGVSVTLARITAGADALIMSRPEPCGLND 705  
 DB 427 VMLGTGCHDLESMLRHEREHNDKRGWGVSVTLARITAGADALIMSRPEPCGLND 705  
 QY 706 YAAAYGVVPVHAHVGVRTVTP-----PPDPFNSGLQPTPRAENKLEALGHC 756  
 DB 487 HANPYGVVPVHSSTGLVDTVYKGYTGFHAGPFDFVCEC-----VDPDDVDKLAATVKA 541  
 QY 757 LRTYRDYKESWGLQERGSQDFSEWHAALYEDVLI 793  
 DB 542 LRTYRDYKESWGLQERGSQDFSEWHAALYEDVLI 793

## RESULT 12

UGST SOLTU

ID UGST SOLTU STANDARD; PRT; 607 AA.

AC Q00775; Q43176;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Granule-bound glycogen [starch] synthase, chloroplast precursor  
 DE (EC 2.4.1.11).  
 GN MAMY OR GESS.  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Aseridae; Iamids; Solanales; Solanaceae; Solanum.  
 OC NCBI\_Taxid=4113;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC STRAIN=cv. AM79.7322;  
 RA MEDLINE=91360072; PubMed=188609;  
 RA van der Leij F.R., Visser R.G.F., Ponstein A.S., Jacobsen E.,  
 RA Feenstra W.J.;

RT "Sequence of the structural gene for granule-bound starch synthase of  
 RT potato (Solanum tuberosum L.) and evidence for a single point  
 RT deletion in the amf allele."  
 RT Mol. Gen. Genet. 228:240-248(1991).

RN [2].  
 RN REVISIONS.  
 RA van der Leij F.R.;  
 RN Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.  
 RC STRAIN=cv. Dongnong 303;  
 RP Dai W.L., Deng W., Cui M., Xiu M., Zhao S.Y., Wang X.M.;  
 RA Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
 RL -1 CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl} (N) =  
 CC -1 UDP + {(1,4)-alpha-D-glucosyl} (N+1).  
 CC -1 PATHWAY: Starch biosynthesis.  
 CC -1 SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.  
 CC -1 SIMILARITY: Belongs to the glycosyltransferase family 1.  
 CC Bacterial/plant glycogen synthase subfamily.

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 CC -----  
 CC EMBL: X58453; CAA41359.1; -  
 CC EMBL: X83220; CAA58220.1; -  
 CC PIR: S16555; YUPOY.  
 CC InterPro: IPR001296; Glyco\_transf.1.  
 CC Pfam: PF00534; Glycosyltransferase; Glycosyltransferase;  
 CC Glycogen biosynthesis; transferase; Glycosyltransferase;  
 CC Transist peptide; Chloroplast; Starch biosynthesis.  
 CC TRANSIT 1 77 CHLOROPLAST.  
 CC CHAIN 78 607 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.  
 CC BINDING 95 95 UDP-GLUCOSE (BY SIMILARITY).  
 CC CONFLICT 130 130 A -> T (IN REF. 3).  
 CC CONFLICT 398 398 I -> V (IN REF. 3).  
 SQ SEQUENCE 607 AA; 66575 MW; 2A377865CRAFA650 CRC64;

Query Match 21.1%; Score 903; D8 1; Length 607;  
 Best Local Similarity 39.8%; Pred. No. 4.1e-43;  
 Matches 206; Conservative 79; Mismatches 174; Indels 64; Gaps 13;

QY 308 MNVYVVAECSPWCKTGLGADVAGALPKALAKGHEWVWVPRYGDYEAADVGRKYYK 367  
 DB 81 MNLIFVGTGVPMHVPCCGV-----PYDGNLVFIANDMHTALPVLKAYRDHGLMOYTR 470  
 QY 368 AAGDMEVNYFAHYIDGVDFVFDAPLFRHROEDIVGSGROEIN-----KMT 415  
 DB 141 VGDSEIVRFHCKGKGVDFVDFHDLFLER---VWGKTGSKLYGPKTGDYRDQLRFS 197  
 QY 416 LFCRAAVEVPMHVPCCGV-----PYDGNLVFIANDMHTALPVLKAYRDHGLMOYTR 470  
 DB 198 LFCRAAVEVPMHVPCCGV-----PYDGNLVFIANDMHTALPVLKAYRDHGLMOYTR 470  
 QY 471 SIMVHNIAHQGRGVDFEFPTELPEHYLEHFRLYD---PVGGEHANYFAAGLKMADQV 526  
 DB 257 VAFCHINIAVQGRNATFDFGLNLPDEFRRSFDPIGVNKKPCGKKINMKWAGILESHRV 316  
 QY 527 VVSPGYLMEKLVKVEG-GMGLHDIIRQNDKMT-KGTYNGIDNMENNEVVDVHLKSDGYT 583  
 DB 317 VVSPGYLMEKLVKVEG-GMGLHDIIRQNDKMT-KGTYNGIDNMENNEVVDVHLKSDGYT 583  
 QY 584 N--FSLGLTDSGKQCKEALQRELGQVADVPPLGFIGRLDGQKVEIITADAMPWISQ 641  
 DB 367 DVKVIITVPAKRLKGLTQAEIGLPVDSIPILGFIGRLDGQKVEIITADAMPWISQ 641  
 QY 642 DVKVIITVPAKRLKGLTQAEIGLPVDSIPILGFIGRLDGQKVEIITADAMPWISQ 641  
 DB 427 DVKVIITVPAKRLKGLTQAEIGLPVDSIPILGFIGRLDGQKVEIITADAMPWISQ 641



QY 702 LNDLYAMAYGVTVVAHVGVRDTPFPDPFNHSGLGMT-----FDRBAHK 748  
 DB 487 LIDHARRIGTVPICSTGSLVDVKE-----GTCFHMGAAPNVEDVDPADYK 537  
 QY 749 LIEALGHCLRTYRDYKESWRGLQERGMQDPSWEHAKLYEDVLL 793  
 DB 538 IYTVARALAVYGL--AFAMIKNCSELSWKEPAKKWETLLL 580

RESULT 13  
 ID UGST SORBI STANDARD; PRT; 608 AA.  
 AC Q4134; P81888;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Granule-bound glycogen [starch] synthase, chloroplast precursor  
 (EC 2.4.1.11).  
 GN MAXY OR WX.  
 OS Sorghum bicolor (Sorghum) (Sorghum vulgare).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCA clade; Panicoideae; Andropogoneae; Sorghum.  
 CX NCBI\_TaxID=4558;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. 12311; TISSUE=seed;  
 RA Hsing Y.C., Liu C., Yu H., Hsieh J.;  
 RL Submitted (APR-1995) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 336-590 FROM N.A.  
 RC TISSUE=Leaf;  
 RX MEDLINE=99083433; PubMed=9866201;  
 RA Mason-Gamer R.J., Weil C.F., Kellogg E.A.;  
 RT "Granule-bound starch synthase: structure, function, and phylogenetic utility";  
 RT Mol. Biol. Evol. 15:1658-1673(1998).  
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + (1,4)-alpha-D-glucosyl(N) =  
 CC -1- UDP + (1,4)-alpha-D-glucosyl(N+1).  
 CC -1- PATHWAY: Starch biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND (BY SIMILARITY).  
 CC -1- SIMILARITY: Belongs to the glucosyltransferase family 1.  
 CC Bacterial/plant glycogen synthase subfamily.  
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 CC -----  
 CC EMBL: U23945; AAC49804.1; -  
 CC EMBL: AF079258; AAD02978.1; -  
 CC DR PIR: T14731; T14731.  
 CC DR InterPro: IPR001296; Glyco\_transf\_1.  
 CC DR Pfam: PF00534; Glycos\_transf\_1; 1.  
 CC KW Glycogen biosynthesis; Transferase; Glycosyltransferase;  
 CC KW Transf peptide; Chloroplast; Starch biosynthesis.  
 CC FT TRANSIT 1 77 CHLOROPLAST (BY SIMILARITY).  
 CC FT CHAIN 78 608 GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE.  
 CC FT BINDING 97 97 UDP-GLUCOSE (BY SIMILARITY).  
 CC FT SEQUENCE 608 AA; 66074 MW; C31333FA87D2D8A6 CRC64;

Query Match 20.7%; Score 883; DB 1; Length 608;  
 Best Local Similarity 40.8%; Pred. No. 5.3e-42;  
 Matches 208; Conservative 72; Mismatches 196; Indels 34; Gaps 10;

QY 308 MNVYVVAACSPWCKTGGIGDVALPKRLARGRHVVVPRYGVDEAYDVGRKYYK 367  
 DB 82 MNVYVVAACSPWCKTGGIGDVALPKRLARGRHVVVPRYGVDEAYDVGRKYYK 367

QY 368 AAGQDMENVYFAHYIDGVDFVFIADPLFRH-----QEDYGSR-----OEIMKMLFC 418  
 DB 142 MGQDEYETRFPHCYKRVADVDFIDHPLFLERVWGKEEIKYGPDACTYDQNLRSLLC 201  
 QY 419 KAAVEVMHNVCCGVPVGGD-----NLVFANIDWHTALLPYLLKAYYRDHGLAQYRSIMV 474  
 DB 202 QALAEAPRILSNPNPFSGPEYGEDVVFVCGNIMHTGSLCYLSNTOGNIYDAKAF 261  
 QY 475 IHNIAHQGRGVDFPEFTELPEHYLHFRLYD-----PVGEHANYEPAGLIMADQVYVS 530  
 DB 262 IHNISYQRFAPSDPELNPFRFKSDFDIDYEKEVEGRKINMMAAGILIEDRLVTVS 321  
 QY 531 PGYLMEL-KTYEGMGWGLHDIIRQNDMKTGRTVNGIDMMENNPEDVALKSDGYTNFSLGT 589  
 DB 322 PYTABELISGARCELDNIRKLTG--ITGIYNDVSEMDPSDKTIA-----VKYDVST 375  
 QY 590 LDSGRQCKEALQRELGQYRADVPLLGFIGRLDQGVETIADAMFVYSQVQVYMLG 649  
 DB 376 AVEAKALNKEALQVEVGLPVDRKIPVAFIGRLEREGQPDVMAAAILDMEEDIQVILG 435  
 QY 650 TGRDLESMLEPHREHHDKRVGVSVRLAHRITGAGALLMPSRFPQGLNQYAMA 709  
 DB 436 TGKKKFERMLMSAEKYPDKRAVAKNAALAHHTMGADLAVTSRFPQGLQLOQMR 495  
 QY 710 YGTVPVVAHVGVRDTPFPDPFNHSGL-----GTFPRAEAKLIEALGHCLRTYRD--Y 763  
 DB 496 YOTPCACASTGSLVDITIEGKTGFHMGRLSVQCNVBPADYKVAATLLKRAIKVGTGPAY 555  
 QY 764 KESWRGLQERGMQDPSWEHAKLYEDVLL 793  
 DB 556 EE---MVYKNCMIQDLSWKGPAKMWENVLL 581

RESULT 14  
 ID UGST WHEAT STANDARD; PRT; 615 AA.  
 AC P27736;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Granule-bound glycogen [starch] synthase, chloroplast precursor  
 (EC 2.4.1.11) (Granule-bound starch synthase) (GBSS).  
 GN MAXY.  
 OS Triticum aestivum (Wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 CC Triticeae; Triticum.  
 CX NCBI\_TaxID=4565;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Endosperm;  
 RX MEDLINE=9132506; PubMed=1863765;  
 RA Clark J.R., Robertson M., Ainsworth C.C.;  
 RT "Nucleotide sequence of a wheat (Triticum aestivum L.) cDNA clone  
 RT encoding the waxy protein";  
 RT Plant Mol. Biol. 16:1099-1101(1991).  
 RN [2]  
 RP SEQUENCE OF 71-78.  
 RC STRAIN=cv. Chinese Spring;  
 RX MEDLINE=93271462; PubMed=8499619;  
 RA Ainsworth C., Clark J., Baleson J.;  
 RT "Expression, organisation and structure of the genes encoding the  
 RT waxy protein (granule-bound starch synthase) in wheat";  
 RT Plant Mol. Biol. 22:67-82(1993).  
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + (1,4)-alpha-D-glucosyl(N) =  
 CC -1- UDP + (1,4)-alpha-D-glucosyl(N+1).  
 CC -1- PATHWAY: Starch biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.  
 CC -1- SIMILARITY: Belongs to the glucosyltransferase family 1.  
 CC Bacterial/plant glycogen synthase subfamily.  
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DR EMBL, X57233, CAA0509.1; -.  
DR PIR, S16261; YUMTY.  
DR InterPro: IPR001296; Glyco trans\_1.  
DR Pfam: PF00534; Glycos transf 1; 1.  
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;  
KW Transf peptide; Chloroplast; Starch biosynthesis.  
FT TRANSIT 1 70 CHLOROPLAST.  
FT CHAIN 71 615 GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE.  
FT BINDING 91 91 UDP-GLUCOSE (BY SIMILARITY).  
SQ SEQUENCE 615 AA; 67751 MW; 87D15F5E1D41D159 CRC64;

Query Match 20.6%; Score 880; DB 1; Length 615;  
Best Local Similarity 40.0%; Pred. No. 7.9e-42;  
Matches 210; Conservative 77; Mismatches 196; Indels 42; Gaps 11;

QY 304 GENANVVVAACSPWCKTGGLGDVAGALPKALAKGHRVWVVPYGYEAYDVGR 363  
DB 73 GSGGNILVFVGAELVAPMSKTGGLDVLGGLPAAVANGHRVWVISPYYDQKAMDTSVI 132  
QY 364 KYKRAAGDMENVYFNAVTDGVDFVIDAPLFRHR-----QEDYGGSR-----QELMKRM 414  
DB 133 SEIKVNDYERKRYRFFCYKRGVDYFDHPFLEKVGKTKKTKYGDAGTIEDNOCRF 192  
QY 415 ILFKAAVEV-----PMHYPCGVPYGDG-NLVFTANDMHTALLPVYLKAY 459  
DB 193 SLCOALAEVPRILDLNNPFPSCGPYAMLGRAVPRRAGEDVVFVCMNHGTLACYLKSN 252  
QY 460 YRDHGLMGTYSIMVHNTIAQGRGPNDEPFTLPEHYLEHFLYD-----PVGGEHANY 515  
DB 253 YQSNQIYFPAKAFCTHNISYQGRSPFDPFQALNLPDFKSSFPFDIGYKPVGRKINW 312  
QY 516 FAAGLKMAQDVVVPYGLVMEIKTEVG-GWGLHDIIRONDWKTRGIYNGIDNEMENPEV 574  
DB 313 MKAGILQADKVLTVSPYAAELISGEARGCELDNIMELTG--ITGIYNGVDVSEMDPIKD 370  
QY 575 VHLKSDGYTNSLGLTDSKQCKEALORELGLOVRADVPILGLTIGLDSGKVEITLADA 634  
DB 371 KFLT-----VNDVDTTALBKALNKEALDAEVLGDPVDRKVPVLAITIGLEEGKGPVMIAA 426  
QY 635 MPMVY-SQDVCLVLTGRHDLSEMLRHFEREHDKVYAGVGFVRLAHRITAGADALLM 693  
DB 427 IDEIYKEDVQVLTGLTKKKKFERLKSEVEKFPKQAVAVRFAAPLAHQWAGADVLAV 486  
QY 694 PSRFPCGILNLYAMAAGTVVVAHVAGVDTVPPEDFPNHSGL-----GWTPEAAEAKL 749  
DB 487 TSRFPCGILQLOGRKYGTPCAGSTGGLVLTIVIEGKTFMGRSLSDVCNVEPADYKV 546  
QY 750 IEALGHCLRTYRDYKESWRGLQERGSQDFSEHAAKLYEDVLK 794  
DB 547 VTTLKRAVAVVG--TPAHHEKAKCMIDLSKSKGAKMEVDLLE 589

## RESULT 15

UGST HORVU STANDARD; PRT: 603 AA.

AC P09842;  
DT 01-MAR-1989 (rel. 10, Created)  
DT 01-MAR-1989 (rel. 10, Last sequence update)  
DT 15-SEP-2003 (rel. 42, Last annotation update)  
DB Granule-bound Glycogen [starch] synthase, chloroplast precursor  
DB (EC 2.4.1.11).  
DB GN MAXY.  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Hordeum.  
OC NCBI\_TaxID=4513;

RM [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Vogelzanger Gold; TISSUE=leaf;  
RX MEDLINE=88303345; PubMed=2970062;  
RA Rhode W., Becker D., Salami F.;  
RT "Structural analysis of the waxy locus from Hordeum vulgare";  
RL Nucleic Acids Res. 16:7185-7186(1988).

RM [2]  
RP SEQUENCE OF 76-89.  
RC STRAIN=cv. H354-295-2-5; TISSUE=Starchy endosperm;  
RX MEDLINE=94170739; PubMed=8125056;  
RA Flengstrand R.;  
RT "Separation of acidic barley endosperm proteins by two-dimensional  
RT electrophoresis";  
RL Electrophoresis 14:1060-1066(1993).  
CC -1- FUNCTION: REQUIRED FOR THE SYNTHESIS OF AMYLOSE IN ENDOSPERM.  
CC -1- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl} (N) =  
CC UDP + {(1,4)-alpha-D-glucosyl} (N+1).  
CC -1- PATHWAY: Starch biosynthesis.  
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.  
CC -1- SIMILARITY: Belongs to the glycosyltransferase family 1.  
CC Bacterial/plant glycogen synthase subfamily.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL, X07931; CAA30755.1; -.  
DR EMBL, X07932; CAA30756.1; -.  
DR PIR, S01727; YUBHY.  
DR InterPro: IPR001296; Glyco trans\_1.  
KW Pfam: PF00534; Glycos transf 1; 1.  
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;  
KW Transf peptide; Chloroplast; Starch biosynthesis.  
FT TRANSIT 1 72 CHLOROPLAST (BY SIMILARITY).  
FT CHAIN 73 603 GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE.  
FT BINDING 90 90 UDP-GLUCOSE (BY SIMILARITY).  
SQ SEQUENCE 603 AA; 66211 MW; 0B0B3DE6A8217934 CRC64;

QY 308 KVVVVVVAACSPWCKTGGLGDVAGALPKALAKGHRVWVVPYGYEAYDVGRKYYK 367  
DB 76 KVLVFGAELVAPMSKTGGLDVLGGLPAAVANGHRVWVISPYYDQKAMDTSVISEIK 135  
QY 368 AAGQDMENVYFNAVTDGVDFVIDAPLFRH-----QEDYGGSR-----QELMKMILFC 418  
DB 136 VADEYERVAFHFCYKRGVDYFDHPFLEKVGKTKKTKYGDAGTIEDNOCRFSLIC 195  
QY 419 KAAYEPMVYPCGVYVYGDG-----NLVFTANDMHTALLPVYLKAYVRDGLMQRSTIV 474  
DB 196 QALLENAPRILNANNPYSGPYGDEVVFCMNHGTLACYLKSNYSIGITRTAKVAF 255  
QY 475 IHNIAQGRGPNDEPFTLPEHYLEHFLYD-----PVGGEHANYFAAGLKRAQDVVVS 530  
DB 256 IHNISYQGRSPFDPFQALNLPDFKSSFPFDIGYKPVGRKINWKGILQADKVLTVS 315  
QY 531 PGYLMELKTEVG-GWGLHDIIRONDWKTRGIYNGIDNEMENPEVYHLKSDGYTNSLGT 589  
DB 316 PYAEELISGEARGCELDNIMELTG--ITGIYNGVDVSEMDPIKXFLA-----VNDIT 369  
QY 590 LDSGKQCKEALORELGLOVRADVPILGLTIGLDSGKVEITLADMPMTV-SQDVCLVWL 648  
DB 370 ALPAKALNKEALDAEVLGDPVDRKVPVLAITIGLEEGKGPVMIAPITLKEEDVQIILL 429  
QY 649 GTRHDLSEMLRHFEREHDKVYAGVGFVRLAHRITAGADALLMPSRFPCGILNLYAM 708

Db 430 GTGKKKFEKLIKSMEEKPGKVRVRFNAPLAHQWAGADLLAVTSRFEPCGLIQLQGM 489  
QY 709 AYGTVPVYHANGVREDTVPFPDPNHSGL----GTFDRAEAHKLIHALGHCLRTYDVK 764  
Db 490 RYGTFCVCASTGGLVDITVEGKTGFHMGRLSDCNVVEPADVKKVAITTLKRAVKVVG--T 547  
QY 765 ESWRGLQERGM SODFSMEHAALYEDVLLK 794  
Db 548 PAYQEMVKNKMIQDLISWKGPAKGMEDVLL 577

Search completed: February 20, 2004, 11:11:48  
Job time : 19 secs



Dd		121	PSMNGTIPVNGKNSITGGGAGATKOSGLPAPRAPHPSTQNRVPVNGENKANVASPFTSTA	180
Qy		181	EVAVPDSSAATISISDKAPESVPAEKPPSPSGSNFVVASAPRLDIDSYEPBLKKGANI	240
Dd		181	EVAVPDSAAATISISDKAPESVPAEKPPSPSGSNFVVASAPRLDIDSYEPBLKKGANI	240
Qy		241	VESAEPKPALSPPAVAVEDLMDPKXTIGEEPEAKODDMAVADAGSFHHQHNDSDG	300
Dd		241	VEEAEPKPALSPPAPAIVEDLMDPKXTIGEEPEAKODDMAVADAGSFHHQHNDSDG	300
Qy		301	PLAGENVMNVVVAACSCPWCKTGGLGDVAGALKPALAKGRHVMVTVPRYDYEAYDY	360
Dd		301	PLAGEVMNVVVAACSCPWCKTGGLGDVAGALKPALAKGRHVMVTVPRYDEEAYDY	360
Qy		361	GVARKYKAAGDMENVYFFAYIDGVDFVFIDAPLFRRHOEDIYGSRROETMKEMILFCXA	420
Dd		361	GVARKYTKAAGDMENVYFFAYIDGVDFVFIDAPLFRRHQEDIYGSFRGEIMKMILLFCXA	420
Qy		421	AWEVPMWPCGGVPYGDANLVFIANDMTALLPVTLKAYTDHGLMQYTSSINVYINIAH	480
Dd		421	AVEVPMWPCGGVPYGDGNLVFIANDMTALLPYVLKAYTDHGLMQYTSSINVYINIAH	480
Qy		481	OQGPGVDEPFPTLPHEYLEHFELRDPVCGSEHANFAAGLKMAQQVWVSFGYLMBELKV	540
Dd		481	OQGPVDEPFPTLPHEYLEHRLVDPROGSEHANFAAGLKMAQQVWVSFGYLMBELKV	540
Qy		541	EGMGJLHDIIIRONDMDKTROIIVNGIDMENRPVYDLKSDGYTPSLGTLDGSKRCKEA	600
Dd		541	EGMGJLHDIIRONDMDKTROIIVNGIDMENRPVYDLKSDGYTPSGLTLDGSKRCKEA	600
Qy		601	LORELGIQVADVPLLGFISGLDDQKGVEIILADAMPVISOVOQLVMJLGTGRHDLSEMLR	660
Dd		601	LORELGIQVADVPLLGFISGLDDQKGVEIILADAMPVISOVOQLVMJLGTGRHDLSEMLR	660
Qy		661	HFEREHDDKTRGVNVSYSVRLAHRTTGADALLMSRFEPCCGALQLYAAVCTVPHVANG	720
Dd		661	HFEREHDDKTRGVNVSYSVRLAHRTTGADALLMSRFEPCCGALQLYAAVCTVPHVANG	720
Qy		721	GVADTVPEPDFNFNSGLGWTFDRABAKHLEALGHCLRTYRDYKESMWGLGERMSODFS	780
Dd		721	GVADTVPEPDFNFNSGLGWTFDRABAKHLEALGHCLRTYRDYKESMWGLGERMSODFS	780
Qy		781	WEBAKLIEBULLKAKYQM 799	
Dd		781	WEBAKLIEBULLKAKYQM 799	
<hr/>				
RESULT 2				
OJLEE3				
ID	OJLEE3	PRELIMITARY;	PRT; 799 AA.	
AC	OJLEE3			
DT	01-OCT-2000 (TREMBLrel_15, Created)			
DT	01-OCT-2000 (TREMBLrel_15, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel_23, Last annotation update)			
DE	Starch synthase Ila-2 precursor (EC 2.4.1.21).			
GN	MS82A-2.			
OS	Triticum aestivum (Wheat).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;			
OC	Triticeae; Triticum.			
OX	NCBI_taxid=4565;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Fielder;			
RA	Gao M., Chibbar R.N.;			
RT	"Isolation, characterization and expression analysis of starch			
RT	synthase Ila cDNA from wheat (Triticum aestivum L.).";			
RL	Submitted (Apr-2000) to the EMBL/GenBank/DDB databases.			
DR	EMBL; AJ269503; CAB96626.1;			
DR	InterPro; IPR001296; Glyco_trans_1.			
DR	Pfam; PF00534; Glycos_transf_1;			
KW	Glycosyltransferase; Transferase; Transit peptide.			

FT	TRANSIT	1	58	POTENTIAL.
FT	CHAIN	59	799	STARCH SYNTHASE IIA-2.
SEQ	SEQUENCE	799 AA;	87278 NM;	50E35CF4B60796CD CRC64;
Query Match		99.6%;	Score 4261;	DB 10; Length 799;
Beet Local Similarity		99.5%;	Pred. No. 2.2e-267;	
Matches	795; Conservative	3;	No. Matches 1;	Indels 0; Gaps 0;
QY		1	MSA VAS A S A S F L A S A S P G R S R R R A R V A D F P H A G A G R L H M P M P P O R T A D G V A A R A	60
DB		1	MSA V A S A S F L A S A S P G R S R R R A R V A S A F F P H A G A G R L H M P M P P O R T A D G V A A R A	60
QY		61	A G K D A R V D D D A A S R O P R A R R G G A T T V A E R D P V K T L D D A A E G G A P A P A P Q D A A R	120
DB		61	A G K D A R V D D D A A S R O P R A R R G G A T T V A E R D P V K T L D D A A E G G A P A P A P Q D A A R	120
QY		121	P S M N G T F V N G E N K S T G G G A T K D S G L P A P A F A P H P S T O N E V P V N G E N K A N A S P P T S I A	180
DB		121	P S M N G T F V N G E N K S T G G G A T K D S G L P A P A F A P H P S T O N E V P V N G E N K A N A S P P T S I A	180
QY		181	E V V A D S A A T T S I S T K A P E S V V A E K P P S S G S N V V A S A P R I D S D V E P E L K K G A V I	240
DB		181	E V V A D S A A T T S I S T K A P E S V V A E K P P S S G S N V V A S A P R I D S D V E P E L K K G A V I	240
QY		241	V E A E N P K A L S P P A A P A V O E D L M D E K K T I G F I E P E A V D G M A V A D D A G S F E H Q N H S G	300
DB		241	V E A E N P K A L S P P A P A V O E D L M D E K K T I G F I E P E A V D G M A V A D D A G S F E H Q N H S G	300
QY		301	P L A G E N N V N V V V V A A E C S P M C K T G E L G V A G L P A L A K R G R V W V V P R Y C D Y E E A Y D V	360
DB		301	P L A G E N N V N V V V A A E C S P M C K T G E L G V A G L P A L A K R G R V W V V P R Y C D Y E E A Y D V	360
QY		361	G V R K T Y K A A G O D M E V N F P H A Y I D G V D F V F I D A P L F R H R O E D I Y G G S R O E I M K R M L L F C K A	420
DB		361	G V R K T Y K A A G O D M E V N F P H A Y I D G V D F V F I D A P L F R H R O E D I Y G G S R O E I M K R M L L F C K A	420
QY		421	A V E V M H N P C G G V P Y G D G N L V F I A N D M T A L P V T L K A Y Y R D H G L M Q T R S I M V I H N I A H	480
DB		421	A V E V M H N P C G G V P Y G D G N L V F I A N D M T A L P V T L K A Y Y R D H G L M Q T R S I M V I H N I A H	480
QY		481	O G R G P V D E P F E L P E S H Y I E H F R L Y D P V G E E I A N T A A G I K A D O Y V V I S P C Y I M E L K T V	540
DB		481	O G R G P V D E P F E L P E S H Y I E H F R L Y D P V G E E I A N T A A G I K A D O Y V V I S P C Y I M E L K T V	540
QY		541	E G S M G L H D I I R O N D M K T R G I V N G I D M E N N P H A V D L K S D G Y T N S I G L T D S G K O C K E A	600
DB		541	E G S M G L H D I I R O N D M K T R G I V N G I D M E N N P H A V D L K S D G Y T N S I G L T D S G K O C K E A	600
QY		601	L O R E I G L O V R A D V P L I G F I G R L D G K V E T I A D A M P I Y S O V O L V M L G T G R H D L E S M R	660
DB		601	L O R E I G L O V R A D V P L I G F I G R L D G K V E T I A D A M P I Y S O V O L V M L G T G R H D L E S M R	660
QY		661	H F E R E H D K Y R G V G S V R L A H R I T A G A D A L M P S F E P C G L N O L Y A M A Y G T V P V H A V G	720
DB		661	H F E R E H D K Y R G V G S V R L A H R I T A G A D A L M P S F E P C G L N O L Y A M A Y G T V P V H A V G	720
QY		721	G V R D I V P R P D P F N H S G L G W T F D P A E A H K I E A L G H C L R T Y R D Y K E S W R G L O E K M S O D P S	780
DB		721	G V R D I V P R P D P F N H S G L G W T F D P A E A H K I E A L G H C L R T Y R D Y K E S W R G L O E K M S O D P S	780
QY		781	W E H A K L Y E D V L L K A K Y Q W	799
DB		781	W E H A K L Y E D V L L K A K Y Q W	799
RESULT 3				
Q8H1Y9	ID	PRELIMINARY;	PRT;	799 AA.
AC	Q8H1Y9;			
DT	01-MAR-2003	(Tremblrel. 23, Created)		
DT	01-MAR-2003	(Tremblrel. 23, last sequence update)		
DT	01-MAR-2003	(Tremblrel. 23, last annotation update)		
DE	Search	synthase II.		

OS Aegilops tauschii (Aegilops squarrosa).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticeae; Aegilops.  
 OC NCBI\_TaxId=37682;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Li Z., Sun F., Chu X., Mukai Y., Yamamoto M., Ali S.,  
 RA Rampling L., Kosar-Harshemi B., Rahman S., Morell M.K.,  
 RA "The structural organization of the gene encoding class II starch  
 RT synthase of wheat and barley, and the evolution of the genes encoding  
 RT starch synthases in plants."  
 RL Funct. Integr. Genomics 0:0-0(2002).  
 DR EMBL; At133248; AAN28308.1;  
 DR SEQUENCE 799 AA; 87014 MW; 68816D82070E2A0B CRC64;

Query Match 95.4%; Score 4078; DB 10; Length 799;  
 Best Local Similarity 95.7%; Pred. No. 1.6e-255;  
 Matches 765; Conservative 6; Mismatches 28; Indels 0; Gaps 0;

QY 1 MSSAVASAFSLALASAPGRSRRRAVSAPPPHAGRLHWPMPPTARTADGVAARA 60  
 DB 1 MSSAVASAFSLALASAPGRSRRRAVSAPPPHAGRLHWPMPPTARTADGVAARA 60  
 QY 61 AGKCDARVDDDAASAROPRARRGGAATKVAEREDPVKTLDRDAEGGAPAPAPRODAAR 120  
 DB 61 AGKCDARVDDDAASAROPRARRGGAATKVAEREDPVKTLDRDAEGGAPAPAPRODAAR 120  
 QY 121 PPSNNGTPVNGENKSTGGGATKDSGLPAPAPAPHPSTQNRVPVNGENKANVASPTSTA 180  
 DB 121 PPSNNGTPVNGENKSTGGGATKDSGLPAPAPAPHPSTQNRVPVNGENKANVASPTSTA 180  
 QY 121 PPSNNGTPVNGENKSTGGGATKDSGLPAPAPAPHPSTQNRVPVNGENKANVASPTSTA 180  
 DB 121 PPSNNGTPVNGENKSTGGGATKDSGLPAPAPAPHPSTQNRVPVNGENKANVASPTSTA 180  
 QY 181 EVVAPDSAAATISIDKAPESVVPAPKPPSSGSNFVVSASAPRLDIDSDVEPELKKGAVT 240  
 DB 181 EVVAPDSAAATISIDKAPESVVPAPKPPSSGSNFVVSASAPRLDIDSDVEPELKKGAVT 240  
 QY 181 EAAASDSAAATISIDKAPESVVPAPKPPSSGSNFVVSASAPRLDIDSDVEPELKKGAVT 240  
 DB 181 EAAASDSAAATISIDKAPESVVPAPKPPSSGSNFVVSASAPRLDIDSDVEPELKKGAVT 240  
 QY 241 VEEAPNPKALSPPAAPAVQEDLMDFKKTYIGFEEPEVEAKDGRAVADAGSFEEHQNHDG 300  
 DB 241 VEEAPNPKALSPPAAPAVQEDLMDFKKTYIGFEEPEVEAKDGRAVADAGSFEEHQNHDG 300  
 QY 301 PLAGENNVVVVVAABCSFCKTGLGADVAGALPKALAKGHRVMVVVPPGYEBAVDV 360  
 DB 301 PLAGENNVVVVVAABCSFCKTGLGADVAGALPKALAKGHRVMVVVPPGYEBAVDV 360  
 QY 301 PLAGENNVVVVVAABCSFCKTGLGADVAGALPKALAKGHRVMVVVPPGYEBAVDV 360  
 DB 301 PLAGENNVVVVVAABCSFCKTGLGADVAGALPKALAKGHRVMVVVPPGYEBAVDV 360  
 QY 361 GVRKTYKAAGDMEVNFHAYIDGVDFVFIAPLFRHROEDIIYGSROEIMKMTLFCCKA 420  
 DB 361 GVRKTYKAAGDMEVNFHAYIDGVDFVFIAPLFRHROEDIIYGSROEIMKMTLFCCKA 420  
 QY 421 AVEVPWNVHPCGGVPPGDDGLVFIANDMTALLPVYLKAYVRDGLMOTRSIMVHNIAH 480  
 DB 421 AVEVPWNVHPCGGVPPGDDGLVFIANDMTALLPVYLKAYVRDGLMOTRSIMVHNIAH 480  
 QY 421 AVEVPWNVHPCGGVPPGDDGLVFIANDMTALLPVYLKAYVRDGLMOTRSIMVHNIAH 480  
 DB 421 AVEVPWNVHPCGGVPPGDDGLVFIANDMTALLPVYLKAYVRDGLMOTRSIMVHNIAH 480  
 QY 481 QGRGVDEFPFTELPEHYLEHFRLYDPVGEHANYFAAGLKNADVVVSPGYLMELKTV 540  
 DB 481 QGRGVDEFPFTELPEHYLEHFRLYDPVGEHANYFAAGLKNADVVVSPGYLMELKTV 540  
 QY 541 EGGWGLHDIIRONDMDKTGIVGIDNMEKNPEVAHLKSDGYTIFSLRTLDGSGRCKEKA 600  
 DB 541 EGGWGLHDIIRONDMDKTGIVGIDNMEKNPEVAHLKSDGYTIFSLRTLDGSGRCKEKA 600  
 QY 601 LQRELGLOVRADVPPLGFIIGRLDGQGYEIIADAMPVIVSODVOLVLMGTGRHDLJESMLR 660  
 DB 601 LQRELGLOVRADVPPLGFIIGRLDGQGYEIIADAMPVIVSODVOLVLMGTGRHDLJESMLR 660  
 QY 661 HFEREHDHVKRGVGFSVRLAHRITAGADALIMPSRFPCGAINOLYAAAYGTIVVAHVG 720  
 DB 661 HFEREHDHVKRGVGFSVRLAHRITAGADALIMPSRFPCGAINOLYAAAYGTIVVAHVG 720  
 QY 721 GVRDVPVPDPFNHSGGLGTFDRABAKLIEALGCLRTYDRYKESWNGLOERGMSODFS 780  
 DB 721 GVRDVPVPDPFNHSGGLGTFDRABAKLIEALGCLRTYDRYKESWNGLOERGMSODFS 780  
 QY 781 WEHAAKLYEDVLKAYQM 799

DB 781 WEHAAKLYEDVLKAYQM 799

# RESULT 4

Q9M466 PRELIMINARY; PRT; 799 AA.

ID Q9M466  
 AC Q9M466  
 DT 01-OCT-2000 (TREMELREL.15, Created)  
 DT 01-OCT-2000 (TREMELREL.15, Last sequence update)  
 DT 01-MAR-2003 (TREMELREL.23, Last annotation update)  
 DE Starch synthase Ila-1 precursor (EC 2.4.1.21).  
 GN MSS2A-1.  
 OS Triticum aestivum (wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticeae; Triticum.  
 OC NCBI\_TaxId=4565;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Fielder;  
 RA Gao M., Chibbar R.N.,  
 RA "Isolation, characterization and expression analysis of starch  
 RT synthase Ila cDNA from wheat (Triticum aestivum L.).",  
 RT Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AJ269502; CAB86618.1;  
 DR InterPro: IPR001296; Glyco. trans. 1.  
 DR Pfam: PF00534; Glycos. trans. 1; 1.  
 KM Glycosyltransferase; Transf. peptidase.  
 FT TRANSIT  
 FT STARCH SYNTHASE Ila-1.  
 FT CHAIN  
 SQ SEQUENCE 799 AA; 86945 MW; 4AD0D20345768A91 CRC64;

Query Match 95.2%; Score 4071; DB 10; Length 799;  
 Best Local Similarity 95.5%; Pred. No. 4.4e-255;  
 Matches 763; Conservative 8; Mismatches 28; Indels 0; Gaps 0;

QY 1 MSSAVASAFSLALASAPGRSRRRAVSAPPPHAGRLHWPMPPTARTADGVAARA 60  
 DB 1 MSSAVASAFSLALASAPGRSRRRAVSAPPPHAGRLHWPMPPTARTADGVAARA 60  
 QY 61 AGKCDARVDDDAASAROPRARRGGAATKVAEREDPVKTLDRDAEGGAPAPAPRODAAR 120  
 DB 61 AGKCDARVDDDAASAROPRARRGGAATKVAEREDPVKTLDRDAEGGAPAPAPRODAAR 120  
 QY 121 PPSNNGTPVNGENKSTGGGATKDSGLPAPAPAPHPSTQNRVPVNGENKANVASPTSTA 180  
 DB 121 PPSNNGTPVNGENKSTGGGATKDSGLPAPAPAPHPSTQNRVPVNGENKANVASPTSTA 180  
 QY 121 PPSNNGTPVNGENKSTGGGATKDSGLPAPAPAPHPSTQNRVPVNGENKANVASPTSTA 180  
 DB 121 PPSNNGTPVNGENKSTGGGATKDSGLPAPAPAPHPSTQNRVPVNGENKANVASPTSTA 180  
 QY 181 EVVAPDSAAATISIDKAPESVVPAPKPPSSGSNFVVSASAPRLDIDSDVEPELKKGAVT 240  
 DB 181 EVVAPDSAAATISIDKAPESVVPAPKPPSSGSNFVVSASAPRLDIDSDVEPELKKGAVT 240  
 QY 181 EAAASDSAAATISIDKAPESVVPAPKPPSSGSNFVVSASAPRLDIDSDVEPELKKGAVT 240  
 DB 181 EAAASDSAAATISIDKAPESVVPAPKPPSSGSNFVVSASAPRLDIDSDVEPELKKGAVT 240  
 QY 241 VEEAPNPKALSPPAAPAVQEDLMDFKKTYIGFEEPEVEAKDGRAVADAGSFEEHQNHDG 300  
 DB 241 VEEAPNPKALSPPAAPAVQEDLMDFKKTYIGFEEPEVEAKDGRAVADAGSFEEHQNHDG 300  
 QY 301 PLAGENNVVVVVAABCSFCKTGLGADVAGALPKALAKGHRVMVVVPPGYEBAVDV 360  
 DB 301 PLAGENNVVVVVAABCSFCKTGLGADVAGALPKALAKGHRVMVVVPPGYEBAVDV 360  
 QY 301 PLAGENNVVVVVAABCSFCKTGLGADVAGALPKALAKGHRVMVVVPPGYEBAVDV 360  
 DB 301 PLAGENNVVVVVAABCSFCKTGLGADVAGALPKALAKGHRVMVVVPPGYEBAVDV 360  
 QY 361 GVRKTYKAAGDMEVNFHAYIDGVDFVFIAPLFRHROEDIIYGSROEIMKMTLFCCKA 420  
 DB 361 GVRKTYKAAGDMEVNFHAYIDGVDFVFIAPLFRHROEDIIYGSROEIMKMTLFCCKA 420  
 QY 421 AVEVPWNVHPCGGVPPGDDGLVFIANDMTALLPVYLKAYVRDGLMOTRSIMVHNIAH 480  
 DB 421 AVEVPWNVHPCGGVPPGDDGLVFIANDMTALLPVYLKAYVRDGLMOTRSIMVHNIAH 480  
 QY 421 AVEVPWNVHPCGGVPPGDDGLVFIANDMTALLPVYLKAYVRDGLMOTRSIMVHNIAH 480  
 DB 421 AVEVPWNVHPCGGVPPGDDGLVFIANDMTALLPVYLKAYVRDGLMOTRSIMVHNIAH 480  
 QY 481 QGRGVDEFPFTELPEHYLEHFRLYDPVGEHANYFAAGLKNADVVVSPGYLMELKTV 540  
 DB 481 QGRGVDEFPFTELPEHYLEHFRLYDPVGEHANYFAAGLKNADVVVSPGYLMELKTV 540

QY 541 EGGWGLHDIIRONDMDKTRGIVNGIDNMENPBYDVLKSDGYTNFSIGTLDGSKRCKEA 600  
 DB 541 EGGWGLHDIIRONDMDKTRGIVNGIDNMENPBYDVLKSDGYTNFSIGTLDGSKRCKEA 600  
 QY 601 LQRELGLQVADVPDLGFGIRLDGQKVEIADAMPWISQDVOLVMLGTGRHDESMR 660  
 DB 601 LQRELGLQVADVPDLGFGIRLDGQKVEIADAMPWISQDVOLVMLGTGRHDESMR 660  
 QY 661 HFERHHDKRGWGFVRLAHRITAGADALLMPSRFGCLNQLYAMAYGTPVVAAG 720  
 DB 661 HFERHHDKRGWGFVRLAHRITAGADALLMPSRFGCLNQLYAMAYGTPVVAAG 720  
 QY 721 GVRDVPFPDPFNHSGIWTGTPDRAEAKLIEALGHCLRTYRDYKESMRGLOERMSODFS 780  
 DB 721 GVRDVPFPDPFNHSGIWTGTPDRAEAKLIEALGHCLRTYRDYKESMRGLOERMSODFS 780  
 QY 781 WEHAKLYEDVLLKAKYQW 799  
 DB 781 WEHAKLYEDVLLKAKYQW 799

## RESULT 5

Q9LEB2 PRELIMINARY; PRT; 798 AA.  
 ID Q9LEB2  
 AC 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Starch synthase Ila-3 precursor (EC 2.4.1.21).  
 CN MS82A-3.  
 OS Triticum aestivum (wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticaceae; Triticum.  
 OC NCBI\_TaxID=4565;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Fielder;  
 RA Gao M., Chidbar R.N.;  
 RT "Isolation, characterization and expression analysis of starch  
 synthase Ila cDNA from wheat (Triticum aestivum L.).";  
 RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AJ269504; CAB96627.1; -  
 DR InterPro: IPR001296; Glycoe\_trans.1.  
 DR Pfam: PF00534; Glycoe\_transf.1; 1.  
 KW Glycosyltransferase; Transferase; Transit peptide.  
 FT TRANSIT 1 58 POTENTIAL.  
 FT CHAIN 59 798 STARCH SYNTHASE IIA-3.  
 SQ SEQUENCE 798 AA; 86794 MW; 8A6CF1F5B716DE4 CRC64;

Query Match 94.9%; Score 4059.5; DB 10; Length 798;  
 Best Local Similarity 95.7%; Pred. No. 2.5e-254;  
 Matches 765; Conservative 8; Mismatches 25; Indels 1; Gaps 1;

QY 1 MSSAVASAASFLALASASPGRRRRARVSAPPFHAGAGRLHMPMPGRTARDGVAAR 60  
 DB 1 MSSAVASAASFLALASASPGRRRRARVSAPPFHAGAGRLHMPMPGRTARDGVAAR 60  
 QY 61 AGKCARVDDDAASAROPARRGGAATVYERRRDVKTLDADAEGGAPAPAPRODAR 120  
 DB 61 AGKCARVDDDAASAROPARRGGAATVYERRRDVKTLDADAEGGAPAPAPRODAR 120  
 QY 61 AGKCARVDDDAASAROPARRGGAATVYERRRDVKTLDADAEGGAPAPAPRODAR 120  
 DB 61 AGKCARVDDDAASAROPARRGGAATVYERRRDVKTLDADAEGGAPAPAPRODAR 120  
 QY 180 EYAAPDPAAATISIDDAPESSVPAEKAPSSGSSNVPSASAPAGSTVSDVELEKKA 239  
 DB 180 EYAAPDPAAATISIDDAPESSVPAEKAPSSGSSNVPSASAPAGSTVSDVELEKKA 239  
 QY 241 VEAPAPKALSPAPAVOEDLWDFKXITGFEEPEYAKDGNVADDAAGSFEEHQNHDG 300  
 DB 241 VEAPAPKALSPAPAVOEDLWDFKXITGFEEPEYAKDGNVADDAAGSFEEHQNHDG 300  
 QY 240 YEAAPKALSPAPAVOEDLWDFKXITGFEEPEYAKDGNVADDAAGSFEEHQNHDG 299  
 DB 240 YEAAPKALSPAPAVOEDLWDFKXITGFEEPEYAKDGNVADDAAGSFEEHQNHDG 299

QY 301 PLAGENMNTVVVAAECSPMCKTGGIGDVAGLLPKALAKGHRVWVVRGYDEBAYDV 360  
 DB 300 PLAGENMNTVVVAAECSPMCKTGGIGDVAGLLPKALAKGHRVWVVRGYDEBAYDV 359  
 QY 361 GVRKTYAAGDNEVNTFAAYITGVDPVFIDALFPRRODITGSSROETKEMILLFCA 420  
 DB 360 GVRKTYAAGDNEVNTFAAYITGVDPVFIDALFPRRODITGSSROETKEMILLFCA 419  
 QY 421 AVEYPMVPCGGVYGGDNVFLANDMHTALLPYLLKAYYRDHGLMQYTSIMVINIAH 480  
 DB 420 AVEYPMVPCGGVYGGDNVFLANDMHTALLPYLLKAYYRDHGLMQYTSIMVINIAH 479  
 QY 481 QGRGPVDEFPPTLPEHYLHFRLYDPVGGHANYFAAGIKMADQVVVSPGYLMEIKTV 540  
 DB 480 QGRGPVDEFPPTLPEHYLHFRLYDPVGGHANYFAAGIKMADQVVVSPGYLMEIKTV 539  
 QY 541 EGGWGLHDIIRONDMDKTRGIVNGIDNMENPBYDVLKSDGYTNFSIGTLDGSKRCKEA 600  
 DB 540 EGGWGLHDIIRONDMDKTRGIVNGIDNMENPBYDVLKSDGYTNFSIGTLDGSKRCKEA 599  
 QY 601 LQRELGLQVADVPDLGFGIRLDGQKVEIADAMPWISQDVOLVMLGTGRHDESMR 660  
 DB 600 LQRELGLQVADVPDLGFGIRLDGQKVEIADAMPWISQDVOLVMLGTGRHDESMR 659  
 QY 661 HFERHHDKRGWGFVRLAHRITAGADALLMPSRFGCLNQLYAMAYGTPVVAAG 720  
 DB 660 HFERHHDKRGWGFVRLAHRITAGADALLMPSRFGCLNQLYAMAYGTPVVAAG 719  
 QY 721 GVRDVPFPDPFNHSGIWTGTPDRAEAKLIEALGHCLRTYRDYKESMRGLOERMSODFS 780  
 DB 720 GVRDVPFPDPFNHSGIWTGTPDRAEAKLIEALGHCLRTYRDYKESMRGLOERMSODFS 779  
 QY 781 WEHAKLYEDVLLKAKYQW 799  
 DB 780 WEHAKLYEDVLLKAKYQW 798

## RESULT 6

Q8H1Y8 PRELIMINARY; PRT; 802 AA.  
 ID Q8H1Y8  
 AC 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Starch synthase II.  
 CN Hordeum vulgare (Barley).  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticaceae; Hordeum.  
 OC NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Himalaya;  
 RA Li Z., Sun F., Xu S., Chu X., Mukai Y., Yamamoto M., Ali S.,  
 RT "The structural organization of the gene encoding class II starch  
 synthase in wheat and barley, and the evolution of the genes encoding  
 starch synthases in plants.";  
 RL Funct. Integr. Genomics 0:0-0(2002).  
 DR EMBL: AY133249; AAN28309.1; -  
 SQ SEQUENCE 802 AA; 87458 MW; 6D08FC195164B46F CRC64;

Query Match 89.5%; Score 3826.5; DB 10; Length 802;  
 Best Local Similarity 90.0%; Pred. No. 3e-239;  
 Matches 730; Conservative 17; Mismatches 43; Indels 21; Gaps 4;

QY 1 MSSAVASAASFLALASASPGRRRRARVSAPPFHAGAGRLHMPMPGRTARDGVAAR 59  
 DB 1 MSSAVASAASFLALASASPGRRRRARVSAPPFHAGAGRLHMPMPGRTARDGVAAR 60  
 QY 60 AGKCARVDDDAASAROPARRGGAATVYERRRDVKTLDADAEGGAPAPAPRODAR 119  
 DB 60 AGKCARVDDDAASAROPARRGGAATVYERRRDVKTLDADAEGGAPAPAPRODAR 119

DB 61 AAG-----IDDAAPGRPARRRYGATKVA---DPVKTLDLDDAAEGGSPSPAPRODAA 111  
 QY RPSMNGTVPNGENKSTGGGATKDSGLPAPAPAPHESTONRVPNGENKAVASPPTSI 179  
 DB 112 RLPSSNGLTLNGENKPTGGGATKDSGLPTAPAPHLISIQNRVPNGENKAKVASPPTSI 171  
 QY 180 AEVAPDSAAATISIDKAPESVPAEKPP-----PSSGSNFVVSASAPRLIDS 228  
 DB 172 VDVASPGSAANISISNKVPPSVPAKTPPSSVPAKTLTPSSGSNFVVSASAPRLIDS 231  
 QY 229 DVEPELKGAVIYEAPNPFKALSPPAPAVOEDLMDFKKTYIGFEEPEAKDGMNAVADA 288  
 DB 232 DVELAQKDALIYKAPKPKALSAPAVOEDLMDFKKTYIGFEEPEAKDGSNAVADA 291  
 QY 289 GSFEHONHDSGPLAGENVVNVVVAACSPWCKTGSGIDVAGALPKALAKGHRVWV 348  
 DB 292 GSFEHONHDSGPLAGENVVNVVVAACSPWCKTGSGIDVAGALPKALAKGHRVWV 351  
 QY 349 PRYGDYEADYDVKRYKKAAGDMEVNTFYAYIDGVDFVTDAPLFRHROEDITYGSSRQ 408  
 DB 352 PRYGDYEADYDVKRYKKAAGDMEVNTFYAYIDGVDFVTDAPLFRHROEDITYGSSRQ 411  
 QY 409 EIMKMIILFCKAAVEVPMHVPCGGVPGDGNLFIANDMHTALLPYLKAYYRDHGLMOY 468  
 DB 412 EIMKMIILFCKAAVEVPMHVPCGGVPGDGNLFIANDMHTALLPYLKAYYRDHGLMOY 471  
 QY 469 TRSIWVHINIAHQGRGVDFEPTTELPEHYLEHFLYDVGGEHANYFAAGLKAAQVYV 528  
 DB 472 TRSIWVHINIAHQGRGVDFEPTTELPEHYLEHFLYDVGGEHANYFAAGLKAAQVYV 531  
 QY 529 VSPGYLMELKTVEGGWGLHDIIRONDWKTRGIYNGIDNMENPEVDVHLKSDGYTFSLK 588  
 DB 532 VSPGYLMELKTVEGGWGLHDIIRONDWKTRGIYNGIDNMENPEVDVHLKSDGYTFSLK 591  
 QY 589 TLDSGKQCKEALQRELGIQVADVPILGFIQLDQKVEIITADAMPVVSQDVQVLM 648  
 DB 592 TLDSGKQCKEALQRELGIQVADVPILGFIQLDQKVEIITADAMPVVSQDVQVLM 651  
 QY 649 GTGRHDLSEMLRHEERHHDKYRGWGFSVRLAHRITAGADALLMSPREPCGINQIYAM 708  
 DB 652 GTGRHDLSEMLRHEERHHDKYRGWGFSVRLAHRITAGADALLMSPREPCGINQIYAM 711  
 QY 709 AYGTVPVVHAGVGRDTPVPFPFNHSGIOWTDRABAHKLEALGHCLRTYRDHESMR 768  
 DB 712 AYGTVPVVHAGVGRDTPVPFPFNHSGIOWTDRABAHKLEALGHCLRTYRDHESMR 771  
 QY 769 GLOERGMSODFSWEHAAKLYEDVILKAKYQW 799  
 DB 772 GLOERGMSODFSWEHAAKLYEDVILKAKYQW 802

RESULT 7  
 08H1Y7 PRELIMINARY; PRT; 802 AA.  
 AC 08H1Y7;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Search synchase II.  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 OC NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Morex;  
 RA Li Z., Sun F., Xu S., Chu X., Mukai Y., Yamamoto M., Ali S.,  
 RA Ramlipati L., Kogari-Harsheni B., Rahman S., Morell M.K.;  
 RA "The structural organization of the gene encoding class II starch  
 RT synthase of wheat and barley, and the evolution of the genes encoding  
 RT starch synthases in plants.";  
 RL Funct. Integr. Genomics 0:0-0(2002).

DR EMBL: AY133251; AAN28307.1; -.  
 DR EMBL: AY133250; AAN28307.1; JOINED.  
 SQ SEQUENCE 802 AA; 87474 MW; 977649133F31E51 CRC64;  
 Query Match 89.3%; Score 3816.5; DB 10; Length 802;  
 Best Local Similarity 89.9%; Pred. No. 1.3e-238;  
 Matches 729; Conservative 17; Mismatches 44; Indels 21; Gaps 4;  
 QY 1 MSSAVASAFALASASPCR--SRRARYSAPPNAGARLAMPMPQRTARDGVAAAR 59  
 DB 1 MSSAVASAFALASASPCR--SRRARYSAPPNAGARLAMPMPQRTARDGVAAAR 60  
 QY 60 AAGKCDARVDDDAASARQPARRGAAATYVARRDPVKTLDSDAEGAPADPAPRODAA 119  
 DB 61 AAG-----IDDAAPGRPARRRYGATKVA---DPVKTLDLDDAAEGGSPSPAPRODAA 111  
 QY 120 RPSMNGTVPNGENKSTGGGATKDSGLPAPAPAPHESTONRVPNGENKAVASPPTSI 179  
 DB 112 RLPSSNGLTLNGENKPTGGGATKDSGLPTAPAPHLISIQNRVPNGENKAKVASPPTSI 171  
 QY 112 AEVAPDSAAATISIDKAPESVPAEKPP-----PSSGSNFVVSASAPRLIDS 228  
 DB 172 VDVASPGSAANISISNKVPPSVPAKTPPSSVPAKTLTPSSGSNFVVSASAPRLIDS 231  
 QY 180 AEVAPDSAAATISIDKAPESVPAEKPP-----PSSGSNFVVSASAPRLIDS 228  
 DB 172 VDVASPGSAANISISNKVPPSVPAKTPPSSVPAKTLTPSSGSNFVVSASAPRLIDS 231  
 QY 229 DVEPELKGAVIYEAPNPFKALSPPAPAVOEDLMDFKKTYIGFEEPEAKDGMNAVADA 288  
 DB 232 DVELAQKDALIYKAPKPKALSAPAVOEDLMDFKKTYIGFEEPEAKDGSNAVADA 291  
 QY 289 GSFEHONHDSGPLAGENVVNVVVAACSPWCKTGSGIDVAGALPKALAKGHRVWV 348  
 DB 292 GSFEHONHDSGPLAGENVVNVVVAACSPWCKTGSGIDVAGALPKALAKGHRVWV 351  
 QY 349 PRYGDYEADYDVKRYKKAAGDMEVNTFYAYIDGVDFVTDAPLFRHROEDITYGSSRQ 408  
 DB 352 PRYGDYEADYDVKRYKKAAGDMEVNTFYAYIDGVDFVTDAPLFRHROEDITYGSSRQ 411  
 QY 409 EIMKMIILFCKAAVEVPMHVPCGGVPGDGNLFIANDMHTALLPYLKAYYRDHGLMOY 468  
 DB 412 EIMKMIILFCKAAVEVPMHVPCGGVPGDGNLFIANDMHTALLPYLKAYYRDHGLMOY 471  
 QY 469 TRSIWVHINIAHQGRGVDFEPTTELPEHYLEHFLYDVGGEHANYFAAGLKAAQVYV 528  
 DB 472 TRSIWVHINIAHQGRGVDFEPTTELPEHYLEHFLYDVGGEHANYFAAGLKAAQVYV 531  
 QY 529 VSPGYLMELKTVEGGWGLHDIIRONDWKTRGIYNGIDNMENPEVDVHLKSDGYTFSLK 588  
 DB 532 VSPGYLMELKTVEGGWGLHDIIRONDWKTRGIYNGIDNMENPEVDVHLKSDGYTFSLK 591  
 QY 589 TLDSGKQCKEALQRELGIQVADVPILGFIQLDQKVEIITADAMPVVSQDVQVLM 648  
 DB 592 TLDSGKQCKEALQRELGIQVADVPILGFIQLDQKVEIITADAMPVVSQDVQVLM 651  
 QY 649 GTGRHDLSEMLRHEERHHDKYRGWGFSVRLAHRITAGADALLMSPREPCGINQIYAM 708  
 DB 652 GTGRHDLSEMLRHEERHHDKYRGWGFSVRLAHRITAGADALLMSPREPCGINQIYAM 711  
 QY 709 AYGTVPVVHAGVGRDTPVPFPFNHSGIOWTDRABAHKLEALGHCLRTYRDHESMR 768  
 DB 712 AYGTVPVVHAGVGRDTPVPFPFNHSGIOWTDRABAHKLEALGHCLRTYRDHESMR 771  
 QY 769 GLOERGMSODFSWEHAAKLYEDVILKAKYQW 799  
 DB 772 GLOERGMSODFSWEHAAKLYEDVILKAKYQW 802

RESULT 8  
 048899 PRELIMINARY; PRT; 732 AA.  
 AC 048899;  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Starch synthase isoform zsfst1-1 (EC 2.4.1.21) (Fragment).



GN ZSSIIA.  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.  
 OC NCBI\_Taxid=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=M64A; TISSUE=Endosperm;  
 RX MEDLINE=98349857; PubMed=9687068;  
 RA Harn C., Knight M., Ramakrishnan A., Guan H., Keeling P.L.,  
 RA Wasserman B.P.;  
 RT "Isolation and characterization of the ZSSIIA and ZSSIID starch  
 RT synthase cDNA clones from maize endosperm.";  
 RL Plant Mol. Biol. 37:639-649(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=M64A; TISSUE=Endosperm;  
 RA Knight M.E., Harn C., Lilley C.E.R., Guan H., Singletary G.W.,  
 RA Mu-Forester C., Wasserman B.P., Keeling P.L.;  
 RT "Molecular Cloning of Starch Synthase I from Maize (M64) Endosperm and  
 RT Expression in E.coli.";  
 RL Plant J. 0:0-0(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=M64A; TISSUE=Endosperm;  
 RX MEDLINE=99117283; PubMed=9917337;  
 RA Imperial-Radosevich J.M., Nichols D.J., Li P., McKean A.L.,  
 RA Keeling P.L., Guan H.;  
 RT "Analysis of purified maize starch synthases IIA and IIB: SS isoforms  
 RT can be distinguished based on their kinetic properties.";  
 RL Arch. Biochem. Biophys. 362:131-138(1999).  
 DR EMBL; AF019296; A013341.1; -  
 DR InterPro; IPR002086; Aldehyde\_dehydr.  
 DR InterPro; IPR001296; Glyco\_transf.1.  
 DR Pfam; PF00534; Glycos\_transf.1.  
 DR PROSITE; PS00687; ALDEHYDE\_DEHYDR\_GLU; 1.  
 DR GlycoSyLtransferase; Transferase.  
 KW NON\_TER  
 FT SEQUENCE 732 AA; 80246 MW; 22946745055D0F3B CRC64;  
 SC  
 Query Match 65.8%; Score 2811.5; DB 10; Length 732;  
 Best Local Similarity 68.2%; Pred. No. 1,4e-173;  
 Matches 550; Conservative 58; Mismatches 116; Indels 83; Gaps 10;

QY 1 MSSAVASAA--FLALASAPGRSRRARVAPPPAGR--LHMPWPQRTARDG 55  
 DB 1 MSSAAVSSSSSTFFLALASAPG-GRRRAVGSFFTTGASLFARWAPPPARRDA 59  
 QY 56 V-AAAAAKDARVDDAASAROPRARRGGAATKVAERDPVKTLDRAAEGGAPAPA 113  
 DB LVRAEAGAGGADAPERSGDAARLPARRNA--VSKRADPLQ----- 99  
 QY 114 PRODAARPPMNGFPPVNGENKSTGGGATKDSGLPARAPRPHSTONRVVNGENKANA 173  
 DB -----PVRGYSATGN-----TAKGAASCONALADVEIKSTYA 134  
 QY 174 SPPPSIAEVAPDSAAITISIDKAPESVPAEKPPSPSSGNFVVASAPRLDIDVEBE 233  
 DB AAPTISIVKFPAPGRKMLIPSGDIAETVLPAPKXHS-----PAVDGDSN---- 180  
 QY 234 LKGAIVIEEAPNPALASPFAA-PAVOEDLMDFKKYGFEPEYEAQDDGAAVDDAGSPE 292  
 DB -----GIAFTVEBVLVEATWDFKTYGFPDEPAKDDSRVAGDDAGSPE 225  
 QY 293 HHQNHDSGLGENVNVVVAACSPWCKTGIGVYAGALPKALAKGRVNVVPRYG 352  
 DB HYGNDSSGLAGENVMNTVVAACSPWCKTGIGVYAGALPKALAKGRVNVVPRYG 285  
 QY 353 DYEAYDVGVRKYKAAQGDMEVNVFAVYIDGVDFVIDAFLPHQEDYIGGSRQEIWK 412  
 DB DYVEAFDMGIRKRYKAGQD-EVNVYFAHFDGVDFVIDAFLPHQDDIYIGGSRQEIWK 345

QY 413 RMILFCKAAVEVMHPCGGVPYDGNLVIANDMHTALLPYLKAYYRDHGLNQYTSRI 472  
 DB RMILFCKVANEVVMHPCGGVCGDGNLVIANDMHTALLPYLKAYYRDHGLNQYTSV 405  
 QY 473 MVHNINAGRGVYDFPTELPENTLEFALYDYPVGHANYPAAGLKADQVYVSPG 532  
 DB LVHNINAGRGVYDFPTELPENTLEFALYDYPVGHANYPAAGLKADQVYVSPG 465  
 QY 533 YLWELKVEGMDLHDIIRQNDMKTGIVNGIDNEMNVEVDVHLKSDGYTNSLGTIDS 592  
 DB YLWELKVEGMDLHDIIRQNDMKTGIVNGIDNEMNVEVDVHLKSDGYTNSLGTIDA 525  
 QY 593 GKQCKEALORELGLQVADVPPLGFTGRLDQKQVEIADAMPVIVQDQVWLGTGR 652  
 DB GKQCKEALORELGLQVADVPPLGFTGRLDQKQVEIADAMPVIVQDQVWLGTGR 585  
 QY 653 HDLESMLRPEREHDHVKRGVGFVRLARRITAGADALIMPSPREPGLNQLYAMAYGT 712  
 DB ADLERPLQHLERHPKVKVGVGFVPMARITAGADVLMVSPREPGLNQLYAMAYGT 645  
 QY 713 VPVVHAAGVRDVPVPPDPENSGLQWTPDPAHKLTEALGHCRTYRDYKESRGIOE 772  
 DB VPVVHAAGVRDVPVPPDPENSGLQWTPDPAHKLTEALGHCRTYRDYKESRGIOE 705  
 QY 773 RGMGSDPSEHAALYEDVLLKAYQW 799  
 DB RGMGSDPSEHAALYEDVLLKAYQW 732

RESULT 9  
 Q944MS PRELIMINARY; PRT; 810 AA.  
 AC Q944MS;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Putative soluble starch synthase II-3.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Eriacoidae; Oryzaceae; Oryza.  
 OC NCBI\_Taxid=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Mu P., Jiang H.W., Dian W.M.;  
 RT "Oryza sativa putative soluble starch synthase II-3.";  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF190939; A016661.1; -  
 DR Gxateme; Q944MS; -  
 DR InterPro; IPR001296; Glyco\_transf.1.  
 DR Pfam; PF00534; Glycos\_transf.1.  
 FT SEQUENCE 810 AA; 88375 MW; 9676434321EAF72 CRC64;  
 SC  
 Query Match 64.7%; Score 2764.5; DB 10; Length 810;  
 Best Local Similarity 66.4%; Pred. No. 1.7e-170;  
 Matches 555; Conservative 75; Mismatches 143; Indels 63; Gaps 20;

QY 208 PPSGSGNFVVSASAPRLDIDSDVEPELKKGAVIEBAPNPKALSPPAABVQEDJMDPK 267  
 DB 219 PPSGSGNFVVSASAPRLDIDSDVEPELKKGAVIEBAPNPKALSPPAABVQEDJMDPK 275  
 QY 268 YIGFEEFVPAK---DDGNAVADDAAGSPFHQNHSDGPIAGNMMVVVVAECSPWCKT 323  
 DB 276 YFDLNPDAEDDDDDDA-DSDASDSETDODDSDGPIAGNMMVVVVAECSPWCKT 334  
 QY 324 GGLGVAGALPKALAKGHRVWVVPYGDYEAVDGVKXYKKAAGDMEVNYFHAID 383  
 DB 335 GGLGVAGALPKALAKGHRVWVVPYGDYEAVDGVKXYKKAAGDMEVNYFHAID 394  
 QY 384 GVDVFIADALFHRQEDYIGSSROEIMKRMILFCKAAVEVPMHVCGGVPYGGDLVFI 443  
 DB 395 GVDVFIADALFHRQEDYIGSSROEIMKRMILFCKAAVEVPMHVCGGVPYGGDLVFI 454  
 QY 444 ANDMHTALLPYLKAYYRDHGLMOTRSIMVHNIAHOGRGVDEPFTLEPEHYLEHR 503  
 DB 455 ANDMHTALLPYLKAYYRDHGLMOTRSIMVHNIAHOGRGVDEPFTLEPEHYLEHR 514  
 QY 504 LYDVGGEHANYPAGLKKADQVYVVSPOGYLMELKTVEGGWGLHDIIRONDWKTRGIVNG 563  
 DB 515 LYDVGGEHANYPAGLKKADQVYVVSPOGYLMELKTVEGGWGLHDIIRONDWKTRGIVNG 574  
 QY 564 IDMMENPEVDVHLKSDGYTNFSLGTLDSGKOCKEALORELGOVRADVPILGFIGRLD 623  
 DB 575 IDMMENPEVDVHLKSDGYTNFSLGTLDSGKOCKEALORELGOVRADVPILGFIGRLD 634  
 QY 624 GOKXVEIADAMPWISQDVQVLMGTGRHDESMILRHEERHDKVKGVSFLAHR 683  
 DB 635 GOKXVEIADAMPWISQDVQVLMGTGRHDESMILRHEERHDKVKGVSFLAHR 694  
 QY 684 ITGADALIMPSPREPGGLNOLYMAAGTVPVHAAGVGVADTVPPEPPEHSGSLGMPFR 743  
 DB 695 ITGADALIMPSPREPGGLNOLYMAAGTVPVHAAGVGVADTVPPEPPEHSGSLGMPFR 754  
 QY 744 AEAHKLIEALGHCHLRTYDYKESWRLQBERGMSODFSWEHAUKLYEDVILKAKYQW 799  
 DB 755 AEAHKLIEALGHCHLRTYDYKESWRLQBERGMSODFSWEHAUKLYEDVILKAKYQW 810

RESULT 10  
 ID 024398 PRELIMINARY; PRT; 491 AA.  
 AC 024398;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DS Starch synthase (Fragment).  
 GN TAAS.  
 OS Triticum aestivum (wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticaceae; Triticum.  
 OX NCBI\_TaxID=4565;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=cv. Florida; TISSUE=Endosperm;  
 RA Walter L., Loez H., Luetzke S.T.;  
 RT "Sequence analysis of a cDNA coding for a starch synthase of wheat."  
 RL Submitted (Aug-1996) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; U66377; AAB17085.1; -  
 DR InterPro; IPR001296; Glyco\_trans\_1.  
 DR Pfam; PF00534; Glycosyltransferase\_1; 1.  
 FT NON\_TER  
 SQ SEQUENCE 491 AA; 55672 MW; 8A04C3DF9514B6B7 CRC64;

Query Match 61.8%; Score 2642; DB 10; Length 491;  
 Best Local Similarity 98.6%; Pred. No. 7, 1e-163;  
 Matches 484; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

309 NVVVVAECSPWCKTGGIAGVAGALPKALAKGHRVWVVPYGDYEAVDGVKXYKKA 368

QY 309 NVVVVAECSPWCKTGGIAGVAGALPKALAKGHRVWVVPYGDYEAVDGVKXYKKA 368

DB 1 NVVVVAECSPWCKTGGIAGVAGALPKALAKGHRVWVVPYGDYEAVDGVKXYKKA 60  
 QY 369 AGDMEVNYFHAIDGVDVFIFADALFHRQEDYIGSSROEIMKRMILFCKAAVEVPMH 428  
 DB 61 AGDMEVNYFHAIDGVDVFIFADALFHRQEDYIGSSROEIMKRMILFCKAAVEVPMH 120  
 QY 429 PCGGVPYGGDLVFIADMHTALLPYLKAYYRDHGLMOTRSIMVHNIAHOGRGVDE 488  
 DB 121 PCGGVPYGGDLVFIADMHTALLPYLKAYYRDHGLMOTRSIMVHNIAHOGRGVDE 180  
 QY 489 PFTELEPEHYLEHRFLDYPVGEHANYPAGLKKADQVYVVSPOGYLMELKTVEGGWGLH 548  
 DB 181 PFTELEPEHYLEHRFLDYPVGEHANYPAGLKKADQVYVVSPOGYLMELKTVEGGWGLH 240  
 QY 549 IIRONDWKTRGIVNGIDMMENPEVDVHLKSDGYTNFSLGTLDSGKOCKEALORELGLQ 608  
 DB 241 IIRONDWKTRGIVNGIDMMENPEVDVHLKSDGYTNFSLGTLDSGKOCKEALORELGLQ 300  
 QY 609 VRADVPILGFIGRLDGOKGVEIADAMPWISQDVQVLMGTGRHDESMILRHEERH 668  
 DB 301 VRADVPILGFIGRLDGOKGVEIADAMPWISQDVQVLMGTGRHDESMILRHEERH 360  
 QY 669 KYRGVGSFVLAHRITGADALIMPSPREPGGLNOLYMAAGTVPVHAAGVGVADTVP 728  
 DB 361 KYRGVGSFVLAHRITGADALIMPSPREPGGLNOLYMAAGTVPVHAAGVGVADTVP 420  
 QY 728 FDPENHSGSLGMPPEBAHKLIEALGHCHLRTYDYKESWRLQBERGMSODFSWEHAUKLY 788  
 DB 421 FDPENHSGSLGMPPEBAHKLIEALGHCHLRTYDYKESWRLQBERGMSODFSWEHAUKLY 480  
 QY 789 EDVILKAKYQW 799  
 DB 481 EDVILKAKYQW 491

RESULT 11  
 ID 094ET4 PRELIMINARY; PRT; 694 AA.  
 AC 094ET4;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DS Soluble starch synthase II-2.  
 GN Oryza sativa (Rice).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wu P., Jiang H.W., Dian W.M.;  
 RA "Rice soluble starch synthase II-2 mRNA."  
 RT Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF395537; AAK81729.1; -  
 DR Gramene; O94ET4; -  
 DR InterPro; IPR001296; Glyco\_trans\_1.  
 DR Pfam; PF00534; Glycosyltransferase\_1; 1.  
 SQ SEQUENCE 694 AA; 75593 MW; F9E908611E40B230 CRC64;

Query Match 55.3%; Score 2365.5; DB 10; Length 694;  
 Best Local Similarity 59.0%; Pred. No. 9, 4e-145;  
 Matches 476; Conservative 79; Mismatches 131; Indels 121; Gaps 15;

1 NSAVAS---AASFALASASPSGRSRRARVSAPPH--AGAG-RLHMPMPPTADG 54  
 1 MSGAHSPPAATLFLNGSSSSPR-RRSRSVSGVWHLYGFGRLH---MERGLVADG 56  
 55 GV--AARAAGKIDARVDDAASAROPRARCGAATKVAERRDPVTLTLDAAEGAPAP 112  
 57 AVVCSASAAG---EDGVAKA-----TKSA----- 79  
 113 ARQDAARPPSNMGTPVNGENKSTGGGATYDSGLPAPARAPSTQNRVNVGENKANV 172

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Db      80 -----GSSKAVAVGSGT-----AKADHVE-----DS 100
Qy      173 ASPPTIAEVPADSAATISIDKAPESVVPKAPKPPSSGSGNFVVSASAPRLDIDSDVEP 232
      101 VSSPKYKRAVAKQNEVVS---RATKSDAPSKPR-----VDPSPAKAKAD--- 146
Qy      233 ELKKAIVIEEADNPALSPPAAPAVOEDIMFKKTIQFEPEVBAODGMVAADAGSE 292
      147 -----GNAQAVESKALDKED-----VGVAEPLKAKADAGDAGAVSSAD 187
Qy      293 HHONHDSGLAGENMNVVVAAGSCPMCKTGGLGVDAGALPKALAKRGRVWVVPVPRG 352
      188 DSEKESGFLAGNNVNVVVAECPCKTGGLGVDVGLPKALARRGRVWVVPVPRG 247
Db      353 DYEAVYDVGRKXYKKAAGQMEVNFHAYIDGVFVIDAPLEFRHROEDIIYGSROELMK 412
      248 EYAEAKDLGVKSKYRVAGDSEVSEYFPAFIDGVDFVFLBAPPRHRNDIIYGSERFDVTK 307
Qy      413 RMLIFCKAAVEPMHVPCCGVPYGGDNLVFIANDMHTALLPVYLKAYYRDHGLMOYTRSI 472
      308 RMLIFCKAAVEPMHVPCCGSIYGDNLVFIANDMHTALLPVCLKAYYRDHGLMOYTRSV 367
Db      473 MVLHNIHQGRGPVDEPFTELEPEHYLEHFRLYDPVGEHANYFAAGLKNADQVVVSPG 532
      368 LVTHNIHQGRGPVDEPFATMDLEPHYIDHFRLYDPVGEHANYFAAGLKNADQVVVSHG 427
Qy      533 YLMEKLTVEGKGLHDIIRQDWKTRGIVNGIDMNNPEVDVHLKSDGYTFSLGTLDS 592
      428 YLMEIKTMDGQWGLHEIINNDWKLQGTVNGIMAEKNPEVDHLDSDGANTFETLDT 487
Db      593 GKQCKEALORELQVRAVDVPLIGFIRLDGQKGYEIIADAMPWIVSDVQLVYLGTR 652
      488 GKQCKEALORQLQVRAVDVPLIGFIRLDHOKGVDIIGDAMPWLAGOVQVYVYLGTR 547
Qy      653 HDLESMTNHFREHNDKVRGWSVTLARITAGDALMPSRPEPCGLNOLYAMAYST 712
      548 PDLEEMRRFSEHNDKVRGWSVQLARITAGDALMPSRPEPCGLNOLYAMAYST 607
Db      713 VPVHAAGVADTVPPDPFNHSGLWTFDRAEAKHLEALGHCLRTYRDYKESWGLQ 772
      608 VPVHAAGVADTVPPDPFNADTGLWTFDRAEAKHLEALGHCLNTYRNYKESWGLQ 667
Qy      773 RQMSODFSWEHAATLYEDVLIKAKYQW 799
      668 RQMSODFSWEHAATLYEDVLIKAKYQW 694
Db      668 RQMSODFSWEHAATLYEDVLIKAKYQW 694

RESULT 12
Q949A6 PRELIMINARY; PRT; 637 AA.
AC Q949A6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Soluble starch synthase 2 (Fragment).
GN SS2.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Proberg C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ308110; CACS9826.1; -.
DR Gramene; O949A6; -.
DR InterPro; IPR001296; Glyco_transf_1.
DR Pfam; PF00534; Glycof_transf_1; 1.
FT NON TER
SC SEQUENCE 637 AA; 69395 MW; 441975C32AB65D97 CRC64;
Query Match 54.7%; Score 2338.5; DB 10; Length 637;

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      Best Local Similarity 66.0%; Pred. No. 4.7e-143;
      Matches 442; Conservative 74; Mismatches 111; Indels 43; Gaps 7;
Qy      135 STGGGATKQSGLPAPARAPHPSTONRVVPG-----ENKANYASPTSIAEVADSDAA 189
      6 SAAGC-----EDGV-ARKAKSAGSSKRVAMQGSTAYADHEDSVSSPKSVKPAVAKONGE 60
Db      190 TISISDAPSSVVPKAPKPPSSGSGNFVVSASAPRLDIDSDVEBELKKAIVIEBAPK 249
      61 VVS---RATKSDAPSKPR-----VDPSPAKAKAD-----GNAQA 94
Qy      250 LSPRAEAVOEDIMFKKTIQFEPEVBAODGMVAADAGSEFHQNHDSGLAGENMNVN 309
      95 VESKALDKED-----VGVAEPLKAKADAGDAGAVSSADSEKESGFLAGPVVN 147
Db      310 VVVVAAGSCPMCKTGGLGVDVAGALPKALAKRGRVWVVPVPRGYDEAVYGVGRKXYKKA 369
      148 VIVVASECSPCKTGGLGVDVAGALPKALARRGRVWVVPVPRGYEYAEAKDLGVKRYVA 207
Qy      370 GQDMENVFHAVIDGVDFVIDAPLEFRHROEDIIYGSROELMKMLIFCKAAVEPMHVP 429
      208 GQDSEVSTFHAVIDGVDFVIDAPLEFRHRENDIIYGERFDVTKMLIFCKAAVEPMHVP 267
Db      430 CGGVVYGGDNLVFIANDMHTALLPVYLKAYYRDHGLMOYTRSIWVTHNIHQGRGPVDF 489
      268 CGGSIVYGDNLVFIANDMHTALLPVYLKAYYRDHGLMOYTRSVLVTHNIHQGRGPVDDF 327
Qy      490 PFTLEPEHYLEHFRLYDPVGEHANYFAAGLKNADQVVVSPGLMEKLTVEGKGLHDI 549
      388 ATMDLEPHYIDHFRLYDPVGEHANYFAAGLKNADQVVVSHGTYLMEIKTMDGQWGLHEI 387
Db      550 IRQDWKTRGIVNGIDMNNPEVDVHLKSDGYTFSLGTLDSGKQCKEALORELQV 609
      388 INHNDWKLQGTVNGIMAEKNPEVDHLDSDGANTFETLDTGKQCKEALORQLQV 447
Qy      610 RADVPLIGFIRLDGQKGYEIIADAMPWIVSDVQLVYLGTRDLSMTNHFREHNDK 669
      448 RQDWPLIGFIRLDHOKGVDIIGDAMPWLAGOVQVYVYLGTRDLEMLRFESEHNDK 507
Db      508 VRGWSVQLARITAGDALMPSRPEPCGLNOLYAMAYGTVPVVHAAGVADTVPP 723
      670 VRGWSVQLARITAGDALMPSRPEPCGLNOLYAMAYGTVPVVHAAGVADTVPP 723
Qy      730 DPFNHSGLWTFDRAEAKHLEALGHCLRTYRDYKESWGLQ 789
      568 DPFADTGLWTFDRAEAKHLEALGHCLNTYRNYKESWGLQ 627
Db      568 DPFADTGLWTFDRAEAKHLEALGHCLNTYRNYKESWGLQ 627
Qy      790 DVLNKAQYQW 799
      628 DVLNKAQYQW 637
Db      628 DVLNKAQYQW 637

RESULT 13
Q48900 PRELIMINARY; PRT; 698 AA.
AC Q48900;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Starch synthase isoform ZSStII-2 (EC 2.4.1.21).
GN ZSStIIb.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=W64A; TISSUE=Endosperm;
RX MEDLINE=98349857; PubMed=9687068;
RA Harn C., Knight M., Ramakrishnan A., Guan H., Keeling P.L.,
RA Wasserman B.P.;
RA "Isolation and characterization of the ZSStIIa and ZSStIIb starch

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RT synthase cDNA clones from maize endosperm.";  
 RL Plant Mol. Biol. 37:639-649(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=M64A; TISSUE=Endosperm;  
 RA Knight M.E., Hahn C., Lilley C.E.R., Guan H., Singletary G.W.,  
 RA Mu-Foresster C., Masserman B.P., Keeling P.L.,  
 RT "Molecular Cloning of Starch Synthase I from Maize (W64) Endosperm and  
 RT Expression in E.coli.";  
 RL Plant J. 0:0-0(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=M64A; TISSUE=Endosperm;  
 RX MEDLINE=99117283; PubMed=9917337;  
 RA Impati-Radoevich J.M., Nichols D.J., Li P., McKean A.L.,  
 RA Keeling P.L., Guan H.;  
 RT "Analysis of purified maize starch synthases IIa and IIb: SS isoforms  
 RT can be distinguished based on their kinetic properties.";  
 RL Arch. Biochem. Biophys. 362:131-138(1999).  
 DR EMBL; AF019297; A013342.1; -  
 DR InterPro; IPR001296; Glyco\_transf.1.  
 DR Pfam; PF00534; Glycos\_transf.1; 1.  
 KM Glycosyltransferase; Transferase.  
 SQ SEQUENCE 698 AA; 75542 MW; A695785D448119D CRC64;  
 Query Match 54.1%; Score 2314.5; DB 10; Length 698;  
 Best Local Similarity 57.9%; Pred. No. 1.9e-141;  
 Matches 468; Conservative 76; Mismatches 145; Indels 119; Gaps 15;

1 MSSAVASAGFLALASAPGSRRAVSA---PPHAG-RLHWP-EWPORTARDG 55  
 1 MPGAISSSSAFLPVASSPRRRGSGAALSYGSAELRLHVARCPQ---DGA 56  
 56 VAAAPAKKARVDDDA---SAROPARRGAATKVAERDVKLDDAAGGAPAP 112  
 57 ASVRAAAPAGGEESEAKSSSQAGAVGSGTAKAV-----DSAPENPLRS 104  
 113 APRODAPRPPMNGTAVNGENKSTGGGATGGLPAPAPAPHPSTONRVNGENKAV 172  
 105 APRQ-----SQSAAMNG---TSGSSASTAPVSGP-KADHPS----- 139  
 173 ASPTSTAEVAVAPDSATITISDPAKPSVPAKPPSSSSNVASAPRLDIDVDP 232  
 140 -----APVTKEIDAS-----AVPEPAG-----DDARP 163  
 233 ELKGAIVIEEAPRPKALSPAPAVOEDLWDFKTYGFEPEAKODGWAVDAGSFE 292  
 164 -----VBS-----IGAPDAADADAAPADAASAP 190  
 293 H-HQNDHSGPLAGENVANVVAEAGSPWCCTGGLGVAGALPRALAKGRHVAVVPR 351  
 191 YDRDNBPGLAGBNVAVVVAEBCAPFCCTGGLGVVVALPRALARRGRHVAVVPR 250  
 352 GDVEAVDVGRKYYKAGADMENVYFAYIDGVDFEIDAPLEPHRHOEDYIGSREIM 411  
 251 GEYEAADLVGRKYYKAGADSEVTHSYIDGVDFEIVAPPKRHHNTTYGGERLDIL 310  
 311 KRMILFCFAVEVPMVAPCGGTGVGDNVFIANDMTALLPVYLKAYRDNGLMOYARS 370  
 412 KRMILFCFAVEVPMVAPCGGTGVGDNVFIANDMTALLPVYLKAYRDNGLMOYARS 471  
 472 TMVHNIAHOGRGVDEPFTLEPHYLEHRLVDVPGSEHANYFAAGLMAOVVAVSP 531  
 371 VLVHNIAHOGRGVDDVDFDLPEHYIDHFKLYDNIIGDSNVFAAGLTAADRVAVSN 430  
 532 GYLWELKTVSGWGLHDIIRQNDKTRIVNGIDNMENPEVDHLKSDGTYNFSGLTD 591  
 431 GYMWELKTVSGWGLHDIIRQNDKTRIVNGIDNMENPEVDHLKSDGTYNFSGLTD 490  
 592 SGKQCKKALORELGLQVRADVPLGLIGRLDGKQVETIADAMPVVSODVCLVMTGTG 651  
 491 TGKQCKKALORELGLQVRADVPLGLIGRLDGKQVETIADAMPVVSODVCLVMTGTG 550

QY 652 RHDIENLRFERHHDHDKVGNVGFSVRLAHTTAGADALIMSPFPCGINTLYAMAYG 711  
 DB 551 RADLEDMIRRFESHSKVAWGFVPLAHRITAGADILIMSPFPCGINTLYAMAYG 610  
 QY 712 TVPVHVAVGVRDVPFPDPFNNHSGLGMTFDEAHNLEBALGHCRTYDYKESWRGLQ 771  
 DB 611 TVPVHVAVGVRDVPFPDPFNNHSGLGMTFDEAHNLEBALGHCRTYDYKESWRACR 670  
 QY 772 ERGMSQPSFWEHNAKLYEDVLLAKYQW 799  
 DB 671 ARGVAEDLSMDHAALYEDVLLAKYQW 698

RESULT 14  
 Q9MAC8 PRELIMINARY; PRT; 792 AA.  
 AC Q9MAC8;  
 DT 01-OCT-2000 (TREMELrel. 15, Created)  
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)  
 DE Putative glycogen synthase.  
 GN T4P3.13 OR AT3G01180.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,  
 RA Roming C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.B.,  
 RA Bowman C.L., White O., Nijman W.C., Fraser C.M.;  
 RT "Arabidopsis thaliana chromosome III BAC T4P3 genomic sequence.";  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Southwick A., Katlin-Neumann G., Nguyen M., Lam B., Miranda M.,  
 RA Palm C.J., Bowser L., Jones T., Bann J., Carninci P., Chen H.,  
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamuya A., Kawai J.,  
 RA Kim C., Lin J., Liu S.X., Narusaka M., Oodera C.S., Quach H.L., Sakurai T.,  
 RA Sakurai T., Satou M., Seki M., Shim P., Yamada K., Shinozaki K.,  
 RA Ecker J., Theologis A., Davis R.W.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Nguyen M., Southwick A., Tripp M., Palm C.J., Jones T., Wu T.,  
 RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,  
 RA Deng J.M., Hayashizaki Y., Huan W.W., Lee J.M., Ishida J., Kamuya A.,  
 RA Kawai J., Kim C.J., Narusaka M., Oodera C.S., Quach H.L., Sakurai T.,  
 RA Satou M., Seki M., Shim P., Tang C.C., Torcuni M., Wong C., Wu H.C.,  
 RA Yamada K., Yu G., Yvan S., Shinozaki K., Ecker J., Theologis A.,  
 RA Davis R.W.;  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC008261; AAP26156.1; -  
 DR EMBL; AY054467; AAK9659.1; -  
 DR EMBL; BR002555; AAC00915.1; -  
 DR InterPro; IPR001296; Glyco\_transf.1.  
 DR InterPro; IPR002114; HP\_Serp\_site.  
 DR Pfam; PF00534; Glycos\_transf.1; 1.  
 DR PROSITE; PS00589; PTS\_HPR\_SER; 1.  
 SQ SEQUENCE 792 AA; 87592 MW; F8C852E4119E670 CRC64;  
 Query Match 50.5%; Score 2161.5; DB 10; Length 792;  
 Best Local Similarity 57.0%; Pred. No. 1.8e-131;  
 Matches 430; Conservative 97; Mismatches 199; Indels 37; Gaps 10;

QY 60 AAGKADARVDDAAS---AARPARRGAAATKVAERDPYKTL-----DDAAGGAPA 110  
 DB 62 AAGSDDEPEDALQATIDSKKVLAMQRNLHQLERKLVSSIKESPPDDDAASAKQ 121  
 QY 111 PPA---PRQDAPRPPMNGTAVNGENKSTGGGATGGLPAP-ARAPHPSTONRVAVN 165

Db 122 ESASVYANATDATKEIMDGDANGSVSPSTYG---KSLISKEPEAKTSPSTESTL--- 173

Qy 166 GEKANVAPSPPTIAEVVAPDSATISIDKPAESVYPAEKPPSSGGSFVVASAPRUD 225

Db 174 -KIRKSSASAVISSPPTSPQKPSDVAATNGKPMSSVVASVDDPPYPPSSVMTSPKTSIP 232

Qy 226 IDSDVEBELKKGAVIEEAPNPRALSPAPAVOEDLWDFKXYIGPEEVEAKDDGMAVA 285

Db 233 VTSRKGKSKSRAGAFMSD-PLPSYLT---KAPQSTMTKEXK-----VEKTPD---YA 278

Qy 286 DDAGSFHHQNDHSGPLAGENVVNVVVAECSPMCKTGGGLGVAGALPKALAKRGHRM 345

Db 279 SSETNEPGKDEKPPPLAGANVMNVIIVAECAPFSKTGSLGVAGALPKSLAKRGHRM 338

Qy 346 VVPRYGDVEEAYDVGRKYKKAQDMENVYFHAVIDGVDFVFIIDAPLFRHROEDIIYGG 405

Db 339 VVPRYAEYEAARGLGRKRYKKAQDMENVYFHAVIDGVDFVFIIDSPERHLSNNIYGG 398

Qy 406 SRQETMKMTIFCGAAVEVPMHTVPCGGVPGDGLVFIANDMTALLPYTLKAYRDHGL 465

Db 399 NRDLILKRMVLFCKAAVEVPMYVPCGGVCGDGLFIANDMTALLPYTLKAYRDHGL 458

Qy 466 MCTRSIMVHINIAHQSGRPVDEPFTELEPEHYLEHRLYDPVGEHANYFAAGLKMADQ 525

Db 459 MKTFRSVLVIHINIAHQSGRPVDEFSYVDLPSHYLDSFKLYDPVGEHFNFAAGLKAABR 518

Qy 526 VVVVSPGYLMBELKTVEGSGMLHDIIRONDMDKRTGIVGIDNMENPEVDVHLKSDGYTNF 585

Db 519 VLTVSHSGYMEVKTLLEGWGLHININENMDKFRGIVANGIDTOENNEFFDIYHSDYTNF 578

Qy 586 SLGLTDSGRCKEALOREIGLOVRADVPLIGFIRLDGQKVEIIDANPMIYSDVOL 645

Db 579 SLENLHIGKPOCKALQKELGIPRPVPLIGFIRLDHOKGVDLIEANPMMSQVOL 638

Qy 646 VMLGTGRHDLDESMRHEFERHNDKVRGNGVSVLARRITAGADALIMPSRFEPCGINOL 705

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Qy 706 YAMAYGTVPVVAHAGVADTVPRPDPEHNSGLGTPRAEAKKLIIEALGCLRTYRDYKE 765

Db 699 YAMAYGTVPVVAHAGVADTVPRPDPEHNSGLGTPRAEAKKLIIEALGCLRTYRDYKE 758

Qy 766 SWRGLQERMSODPSMEHAKLYEDVILKAKYQW 799

Db 759 SWRGLQERMSODPSMEHAKLYEDVILKAKYQW 792

RESULT 15

QSPH5 PRELIMINARY; FRT; 751 AA.

AC QSPH5; 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-MAY-2000 (Tremblrel. 23, Last annotation update)

DE Granule bound starch synthase II precursor.

GN GBSSTI.

OS Manihot esculenta (Cassava) (Manioc).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Malpighiales; Euphorbiaceae; Manihot.

OX NCBI\_TaxID=3983;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. M.col 22, TISSUE=Tubercous root;

RA Munyikwa T.R.I., Jacobsen E., Visser R.G.F.;

RT "Developmental regulation of cassava granule bound starch synthase II."

RT Aff. J. Root Tuber Crops 2:116-120(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. M.col 22, TISSUE=Tubercous root;

RA Munyikwa T.R.I., Jacobsen E., Visser R.G.F.;

RT Submitted (JUL-1999) to the EMBL/GenBank/DBCP databases.

DR EMBL; AF173900; AAFL13168.1; -.  
DR Interpro; IPR001296; Glyco\_transf\_1.  
DR Pfam; PF00534; Glycos\_transf\_1; 1.  
KW Transil peptide.  
FT CHAIN 1 41 POTENTIAL.  
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GRANULE BOUND STARCH SYNTHASE II.

Query Match 49.2%; Score 2105.5; DB 10; Length 751;  
Best Local Similarity 59.4%; Pred. No. 7.2e-128;  
Matches 403; Conservative 78; Mismatches 134; Indels 63; Gaps 7;

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Qy 217 VSASAPRUDSDVEBELKKGAVIEEAPNPRALSPAPAA--VOEDLWDFKXYIGFEE 273

Db 152 HST-----ADEVSETASSAINRGAKDKDELQCHASPRIAFVKNSTQPKF----- 197

Qy 274 PVEAKDDGMAVADDAAGF-----EHHQNDHG-----P 301

Db 198 ----NDSEKQTDLPSTLSTTDTSTINEBNSHSESTSPMTDIESDSMTEDMKPP 253

Qy 302 IAGENVNVVVAECSFMCCTGGLGVAGALPKALAKRGHRVNVVPRYGDVEEAYDVG 361

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Qy 362 VRKYTKAAGDMENVYFHAVIDGVDFVFIIDAPLFRHROEDIIYGGSRQETMKMTIFCGAA 421

Db 314 VAKRYKVDGQFESYFAFIDGVDFVFIIDSPFRHIGNDIYGNRMDIKRMVLFCKAA 373

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Db 374 VEPVMPVPCGGVPGDGLVFIANDMTALLPYTLKAYRDHGLMOYTRSIMVHINIAHQ 433

Qy 482 GRGVPDEPFTELEPEHYLEHRLYDPVGEHANYFAAGLKMADQVNVVSPGYLMBELKTV 541

Db 434 GRGPGSDFSYVGLPEHYLIDLFKLDHPDGLGDFHFNIPAPELKADRVVYVSHGIAWELKTS 493

Qy 542 GGMGLHDIIRONDMDKRTGIVGIDNMENPEVDVHLKSDGYTNFSLGLTDSGRCKEAL 601

Db 494 GGMGLHDIIRONDMDKRTGIVGIDNMENPEVDVHLKSDGYTNFSLGLTDSGRCKEAL 553

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Db 554 QNELRFAIPRPDVPIGFIIRLDYQKGVDLIEANPMVGOVOLVMLGTGRHDLDESMR 613

Qy 662 FERHNDKVRGNGVSVLARRITAGADALIMPSRFEPCGINOLYAMAYGTVPVVAHAGV 721

Db 614 FERHNDKVRGNGVSVLARRITAGADALIMPSRFEPCGINOLYAMAYGTVPVVAHAGV 673

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Job time : 47 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 22, 2004, 13:48:44 ; Search time 10611 Seconds

(without alignments)  
11608.793 Million cell updates/sec

Title: US-10-018-418-3

Perfect score: 2842

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: gb\_pl:\*  
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13: gb\_un:\*  
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26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vi:\*  
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31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
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37: em\_htg\_vrt:\*  
38: em\_htg\_vrt:\*  
39: em\_hgo\_hum:\*  
40: em\_hgo\_mus:\*  
41: em\_hgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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3	2479.4	87.2	2793	8 TA0269504	AJ269504 Triticum
4	2392.2	84.2	2825	6 A93354	A93354 Sequence 5
5	2382.2	84.2	2825	6 AR174878	AR174878 Sequence
6	2382.2	84.2	2825	6 BD008449	BD008449 Nucleic a
7	2380.6	83.8	2825	8 TA0269502	AJ269502 Triticum
8	2177.4	76.6	2972	8 AY133249	AY133249 Hordeum v
9	1532	53.9	1742	8 TA066377	U66377 Triticum ae
10	1294.8	45.6	2959	8 AF419099	AF419099 Oryza sat
11	1293.2	45.5	2919	8 AK101978	AK101978 Oryza sat
12	1246	43.8	2248	6 BD249572	BD249572 Modificat
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15	1245.2	43.8	2248	6 AR340018	AR340018 Sequence
16	1245.2	43.8	2248	6 BD249569	BD249569 Modificat
17	1245.2	43.8	2248	6 AR340017	AR340017 Sequence
18	1238.6	43.6	2412	6 AX755428	AX755428 Sequence
19	1233.2	43.4	2010	6 BD071186	BD071186 Plant 11k
20	1233.2	43.4	2010	6 AF019296	AF019296 Zea mays
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22	1104.6	38.9	2007	6 A63309	A63309 Sequence 2
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33	972.6	34.2	3856	8 AY133250S2	AY133251 Hordeum v
34	951	33.5	966	8 BT009011	BT009011 Triticum
35	912.2	32.1	2380	6 AR049921	AR049921 Sequence
36	912.2	32.1	2478	6 A63310	A63310 Sequence 3
37	886.6	31.2	1609	8 AK061803	AK061803 Oryza sat
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39	746.2	26.3	4422	8 AY423717	AY423717 Oryza sat
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DEFINITION Triticum aestivum starch synthase IIA mRNA, complete cds.  
ACCESSION AF155217  
VERSION AF155217.2 GI:5834420  
KEYWORDS  
SOURCE  
ORGANISM Triticum aestivum (bread wheat)  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poaceae; Triticaceae; Triticum.  
1 (bases 1 to 2842)  
Li,Z., Chu,X., Mouille,G., Yan,L., Kosar-Hashemi,B., Hey,S.,  
Napier,J., Shewry,P., Clarke,B., Appels,R., Morell,M.K. and



TITLE Rahman, S.  
The localization and expression of the class II starch synthases of  
wheat  
JOURNAL Plant Physiol. 120 (4), 1147-1156 (1999)  
MEDLINE 99373402  
PUBMED 10444098  
REFERENCE 2 (bases 1 to 2842)  
AUTHORS Li, Z., Chu, X., Mouille, G., Yan, L., Kosar-Hashemi, B., Hey, S.,  
Napier, J., Shewry, P., Clarke, B., Appels, R., Morell, M.K. and  
Rahman, S.  
TITLE Direct Submission  
JOURNAL Submitted (30-MAY-1999) CSIRO Division of Plant Industry, GPO Box  
1600, Canberra, ACT 2601, Australia  
3 (bases 1 to 2842)  
AUTHORS Li, Z., Chu, X., Mouille, G., Yan, L., Kosar-Hashemi, B., Hey, S.,  
Napier, J., Shewry, P., Clarke, B., Appels, R., Morell, M.K. and  
Rahman, S.  
TITLE Direct Submission  
JOURNAL Submitted (07-SEP-1999) CSIRO Division of Plant Industry, GPO Box  
1600, Canberra, ACT 2601, Australia  
Sequence update by submitter  
On Sep 7, 1999 this sequence version replaced gi:5825479.  
REMARK COMMENT  
FEATURES  
Source location/Qualifiers

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## ORIGIN

Query Match 100.0%; Score 2842; DB 8; Length 2842;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2842; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGCCACCACTTCGCTGCGCGCTCTGGGGGAGAGAACACCGCGCATGTATCC 60  
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QY 61 ATGCGCGCGCGCATTCGCGCGCGCGCATGTCTGCGCGGTCCGCGCGCGCTCTT 120  
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 Isolation, characterization, and expression analysis of starch  
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 Genome 43 (5), 768-775 (2000)  
 MEDLINE  
 PUBMED  
 20532216  
 11081966  
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 Direct Submission  
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LOCUS Triticum aestivum mRNA for starch synthase I1a-3 (ws82a-3 gene).  
DEFINITION  
AJ269504  
ACCESSION  
AJ269504 1 GT:8951572

KEYWORDS starch synthase; ws82a-3 gene.  
SOURCE Triticum aestivum (bread wheat)  
ORANISM Triticum aestivum  
REFERENCE  
AUTHORS Gao, M. and Chibbar, R.N.  
TITLE Isolation, characterization, and expression analysis of starch synthase I1a cDNA from wheat (Triticum aestivum L.)  
JOURNAL Genome 43 (5), 768-775 (2000)  
MEDLINE 20532216  
PUBMED 11081966  
REFERENCE  
AUTHORS Chibbar, R.N.  
TITLE Direct Submission  
JOURNAL Submitted (05-APR-2000) Chibbar R.N., Cereal Biotechnology, Plant Biotechnology Inst., Natl. Research Council Canada, 110 Gymnasium Place, Saskatoon, Saskatchewan, S7N 0W9, CANADA  
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VERSION ARI74878.1 GI:17915198  
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Unclassified.  
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Block.M., Lotz.H., Intuticke.S., Walter.L., Froberg.C. and

TITLE Kosztan, J.  
Nucleic acid molecules encoding enzymes from wheat which are  
Involved in starch synthesis  
JOURNAL Patent: US 6307125-A 5 23-Oct-2001;  
FEATURES Location/Qualifiers  
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## ORIGIN

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REFERENCE  
 1 Gao, M. and Chibbar, R.N.  
 TITLE Isolation, characterization, and expression analysis of starch synthase I1a cDNA from wheat (Triticum aestivum L.)  
 JOURNAL Genome 43 (5), 768-775 (2000)  
 MEDLINE 20532216  
 PUBMED 11081966  
 2 (bases 1 to 2866)  
 Chibbar, R.N.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-APR-2000) Chibbar R.N., Cereal Biotechnology, Plant Biotechnology Inst., Natl. Research Council Canada, 110 Gymnasium Place, Saskatoon, Saskatchewan, S7N 0W9, CANADA

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ORIGIN

Query Match 83.8%; Score 2380.6; DB 8; Length 2866;  
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 ORGANISM  
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 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Trilicaceae; Trilicium.  
 1 (bases 1 to 1742)  
 Walter, L., Loefer, H. and Luetzel, S.T.  
 Sequence analysis of a cDNA coding for a starch synthase of wheat  
 Unpublished  
 2 (bases 1 to 1742)  
 Walter, L., Loefer, H. and Luetzel, S.T.  
 Submitted (08-AUG-1996) Centre for Applied Molecular Biology of the  
 Plant, University of Hamburg, Ohmhorststrasse 18, Hamburg 22609,  
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LOCUS			linear
DEFINITION		Oryza sativa putative soluble starch synthase II-3	mRNA, complete cds.
ACCESSION	AF419099		
VERSION	AF419099.1	GI:16265833	
KEYWORDS			
SOURCE			
ORGANISM		Oryza sativa	
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.	
REFERENCE		1. (bases 1 to 2959)	
AUTHORS		Wu, P., Jiang, H.W. and Dian, W.M.	
TITLE		Oryza sativa putative soluble starch synthase II-3	
JOURNAL		Unpublished	
REFERENCE		2. (bases 1 to 2959)	
		Wu, P., Jiang, H.W. and Dian, W.M.	
		Direct Submission	
		Submitted (11-SEP-2001) Institute of Plant Science, College of Life Sciences, Zhejiang University, Kexiuan Road 266#, Hangzhou, Zhejiang	
		Province 310029, P.R. China	
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## ORIGIN

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Query Match 45.6%; Score 1294.8; DB 8; Length 2959;  
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 Matches 1762; Conservative 0; Mismatches 654; Indels 30; Gaps 5;

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Oy	2204	TACGCGATGAGCTAAGCGAACCGTCCCCTGCTGACGCGCTGCGGGGTGAGCGACCC		2263
Oy	2352	TACGCGATGAGCTAAGCGAACCGTCCCCTGCTGACGCGCTGCGGGGTGAGCGACCC		2411
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AKI01978				
LOCUS				
DEFINITION	AKI01978	2919 bp	mRNA	linear
	Oryza sativa (japonica cultivar-group)		CDNA clone J033076P09, full	PLN 24-JUN-2003
	insert sequence.			
ACCESSION	AKI01978			
VERSION	AKI01978.1	GI:32987187		
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SOURCE	Oryza sativa (japonica cultivar-group)			
ORGANISM	Oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartidae; Oryzaceae; Oryza.			
REFERENCE	1	The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team, Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yarak,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Nemiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohnuki,K., Shienki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Okano,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tanoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Naikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Mikura,J., Ikeda,R., Ishibiki,Y., Kawamata,M., Yoshimura,A., Matsuura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN, Kawai,J., Carninci,P., Adachi,U., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Kono,H., Miyazaki,A., Osato,N., Ota,Y., Saito,S., Saeki,D., Sato,K., Shibata,K., Shingawa,A., Shiraki,T., Yoshino,M., and Hayashizaki,Y. Collection, mapping, and annotation of over 28,000 cDNA clones from Japanese rice		
TITLE	Science 301 (5631), 376-379 (2003)			
JOURNAL	2 (bases 1 to 2919)			
MEDLINE	22752273			
PUBMED	12869764			
REFERENCE				
AUTHORS	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiroaka,T., Hori,F., Hotta,I., Iida,Y., Iida,Y., Ikeda,R., Imanishi,K., Imotani,K., Ishibiki,Y., Ishii,Y., Ishikawa,M., Itoh,H., Kagawa,I., Kawagawa,S., Katoh,H., Kawagashira,T., Kawai,T., Kawabata,M.,			

Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurotsaki, T., Kusumegi, T., Li, C., Lu, M., Maeda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Morikami, K., Murata, M., Nagata, T., Nakamura, M., Natsuki, T., Nariikawa, R., Niihara, J., Nishi, K., Nomura, K., Ohsato, N., Obe, Y., Ohtomo, Y., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Obe, Y., Ohtomo, Y., Ryū, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shimagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takahashi, S., Takata, T., Tomaru, A., Toy, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yatake, J., Yokomizo, S. and Yoshimura, A.  
 Direct Submission  
 Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kamondai, Tsukuba, Ibaraki 305-8602 Japan (E-mail: skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)  
 This clone is one of the 26K full-length cDNA clones from japonica rice.  
 URL : <http://cdna01.dna.affrc.go.jp/cDNA/>  
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satch, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Nishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Nami, T., Ohnada, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.  
 FAIS Genome Sequencing & Analysis: Ohtomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurotsaki, T., Kusumegi, T., Lu, M., Maeda, H., Miura, J., Mizuno, K., Nariikawa, R., Niihara, J., Oka, M., Ryū, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.  
 Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aikawa, K., Akimura, T., Arikawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Itoh, K., Ito, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kaga, T., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohtomo, N., Osato, N., Oka, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shimagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Kohashi, S., Tanaka, F., Tomaru, A., Toy, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.  
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QY	299	GAGCGCGCTCTCCGAGAGGACGCCCGCGGACAGCCCGCGGTGAGCCCGCCACCAAGTTCGCG	358
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QY	359	GAGCGAGAGGATCCCGTTCAGAGCGCTTGATTCGGAACGCCCGGAGAGGTGGCCGCGGCA	418
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QY	1424	GATTGGCAACCGGACATCTGCCGTGTATCTGAAGCAATATTACAAGGACATGTGTTG	1483
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QY	2324	GCGCACAACTGATGAGGCGCTCGGCGATCTCCGCACTTACCGGAGACTACAAAGAG	2383
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RESULT 12  
BD249574  
LOCUS  
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JOURNAL  
COMMENT

BD249574 2248 bp DNA linear PAT 17-JUL-2003  
Modification of starch biosynthesis enzyme gene expression for  
production of starch in grain crops.  
BD249574  
BD249574.1 GI:33059344  
JP 2002525029-A/20.  
Zea mays  
Zea mays  
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1 (bases 1 to 2248)  
Broglie, K.E. and Lighner, J.E.  
Modification of starch biosynthesis enzyme gene expression for  
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Parent: JP 2002525029-A 20 13-AUG-2002;  
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PR 28-JUL-1998 US 60/094436  
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PC A01H5/00, A01H1/00, C08B33/00, C12N15/09, C12N15/00 CC  
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AR340022

LOCUS AR340022 2248 bp DNA linear PAT 17-AUG-2003

DEFINITION Sequence 20 from patent US 6570008.

ACCESSION AR340022

VERSION AR340022.1 GI:33731316

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2248)

AUTHORS Brogile, K.E. and Lightner, J.E.

TITLE Modification of starch biosynthetic enzyme gene expression to produce starches in grain crops

JOURNAL Patent: US 6570008-A 20 27-MAY-2003;

FEATURES

location/Qualifiers

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ORIGIN

Query Match 43.8%; Score 1246; DB 6; Length 2248;

Best Local Similarity 84.6%; Pred. No. 7,7e-147;

Matches 1399; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

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Db 553 CTCTACAGATTGAACCATTAAGTACAGAGAGCCACTTGGGATTTCAAGAAATACATTGGCT 612

Qy 900 TCGAGAGAGCCGCTGAGAGCCAGAGATGATGGCTGGGCTGTGACAGATGATCGGGCTCT 959

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Qy 1800 CCGAGGTGAGCGTCCACCTCAAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1859

Db 1513 CCAAGGTGAGCGTCCACCTCAAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1572

Qy 1860 ACTCCGAGAGCGGAGTGTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1919

Db 1573 AGGCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1632

Qy 1920 CCGAGGTGAGCGTCCACCTCAAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1979

Db 1633 CCAAGGTGAGCGTCCACCTCAAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1692

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Qy 2040 GCGGAG 2099

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Qy 2100 GCGGAG 2159

Db 1813 GCGGAG 1872

Qy 2160 TCGTATGAGCGCTCCGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2219

Db 1873 TCGTATGAGCGCTCCGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1932

Qy 2220 GCAACGCTCCGCTGTGAG 2279

Db 1933 GCAACGCTCCGCTGTGAG 1992

Qy 2280 CCTTCAACCACTCCGCGCTCGGGTGAACGTTTCAGACCGCGCGGCAAGCTGATCG 2339

Db 1993 CGTTACAGCAACCGCGGCTCGGGTGAACGTTTCAGACCGCGCGGCAAGCTGATCG 2052

Qy 2340 AGGCGCTCGGGCACTGCTCCGACCTACCGGAGCTACAGAGAGAGCTGGAGGGGCTTC 2399



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Accession	Sequence	Position
Db	AGGCGCTCAAGGCACTGCTCCGACACAGTACCGGAACCTACAGAGAGACCTGAAAGAGCTTC	2112
Db	205, AGGCGCTCAAGGCACTGCTCCGACACAGTACCGGAACCTACAGAGAGACCTGAAAGAGCTTC	2112
Qy	AGGAGGCGGGCAGTATGCGAGAGACTCAAGCTGGAGCATGCGCGCAAGCTCTAGAGAGC	2459
Db	2113 AGGCGGCGCGCATGTGCGAGACCTCACTGGAGACACAGCGGCTAGAGCTTACAGAGAC	2172
Qy	2460 TCTCTCTAAGGCAAGTACCAAGTGTAAAGCT	2493
Db	2173 TCTTGTCAAGGCAAGTACCAAGTGTAAAGCT	2206

RESULT 14	1798 bp	DNA	linear	PAT 17-JUL-2003
BD249570/c				
LOCUS	BD249570			
DEFINITION	Modification of starch biosynthesis enzyme gene expression for production of starch in grain crops.			
ACCESSION	BD249570			
VERSION	BD249570.1			
KEYWORDS	GI:33059340			
SOURCE	CP 2002525029-A/16.			
ORGANISM	Zea mays			
	Zea mays			

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 1798)	Broglie, K. E. and Lightner, J. E.	Modification of starch biosynthesis enzyme gene expression for production of starch in grain crops	Patent: JP 2002535029-A 16 11-AUG-2002; EI DU PONT DE NEMOURS AND CO	OS Zea mays (maize)

PF	25-JUL-1999 JP	200562537
PR	28-JUL-1998 US	60/094436
PI	KAREN E BROGLIE, JONATHAN EDWARD LIGHTNER	
PC	A01H5/00 A01H1/00 C08B33/00 C12N15/09, C12N15/00 CC	
Modification of starch biosynthesis enzyme		
gene expression for		
CC	production	
CC	of starch in grain crops	
PH	Key	Location/Qualifiers
FT	source	1. 1/98
FT		/organism='Zea mays (maize) '.

FEATURES	location/Qualifiers
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## ORIGIN

Query Match	43.8%	Score 1245.2;	DB 6;	Length 1798;
Best Local Similarity	84.5%	Pred. No. 1e-146;		
Matches 1397; Conservative	2;	Mismatches 255;	Indels 0;	Gaps 0

QY	84	CGCGCCTGAGCCCCCGCTGTACAGAAAGCCTTTGGAACTTCAAGAAATACATGGCT	899
Db	1596	CTCTTACAGTTGAGCCATTAGTACAGAGGCCACTTGGATTTCAAGAAATACATGGCTT	1633
QY	900	TCGAGAGACCCGTTGAGAGCCAGAGATGATGGCTGTTCAGATGATGCGGCTCCT	959
Db	1536	TTGACAGCCTTGACGAGGAGAGATGATCCAGGGTTGGTGCAGAGATGCGGTCTT	1577
QY	960	TTGACATCATCCAGAACCATGATTCGAGACCTTTGGCAGGGAGAACGTCATCAACGTGG	1015
Db	1576	TTGACATCATGAGGACCATGATTTCTGGGCCCTTTGGCCGGGAGAAATGTTATACGTA	1511
QY	1020	TCGCGCGAGGCTGCTGAGATGTTCTCCCTGGTGAAACAAGGCGCTTGGAGATGGTCGG	1077
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QY	1080	GTCGTTTGCCAAAGCCTTTGGCGAAGAGGACATCGTGTATGGTTGTGTACCAAGGT	1133

Db	145	GAGCTTACCCAGAGCTTTAGCCGAGAAAGAGGACATCGTGTATGGTTGGTGGTACCAAGT	1397
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Db	1396	ATGGGGACATATGGAGACCTTGTGATATGGAAATCCGAAATATCTCAAGAGCTGACGAC	1337
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Qy	1920	CCGACGTGCGCTGCTGGCTTCAATCGGCGGCTGTGACCGGCGAGAGGGCGTGTGAGATCA	1979
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Qy	2100	GGCGGATGAGGTGAGTTCTCGTGTGCGCTGTGAGCGCACCGGATCAAGGCGGCGCGACGCG	2159
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Db 316 GCACCGTCCCGCTGCTGACAGCCGCTGGCGGGGTGAGGACACCTGCGCCGCTTGAC 257  
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QY 2400 AGAGCGCGGATGTCGACGACCTTACGCTGGAGCATGCGCGCAAGCTTACAGAGAG 2459  
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LOCUS AR340018  
DEFINITION Sequence 16 from patent US 6570008.  
ACCESSION AR340018  
VERSION AR340018.1 GI:33731312  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1798)  
AUTHORS Broglie, K.E. and Lightner, J.E.  
TITLE Modification of starch biosynthetic enzyme gene expression to  
JOURNAL produce starches in grain crops  
FEATURES  
source Location/Qualifiers  
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Query Match 43.8%; Score 1245.2; DB 6; Length 1798;  
Best Local Similarity 84.5%; Pred. No. 1e-146;  
Matches 197; Conservative 2; Mismatches 255; Indels 0; Gaps 0;

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Db 316 GCACCGTCCCGTCTGAGAGCGCGTGGGAGGAGACACCGTCCCGCTTGAGC 257  
QY 2280 CCTTCAACATCTCGGCTGAGGAGCTTGAACCGCGCCAGAGGCGCAAGCTGATG 2339  
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Mon Feb 23 11:51:11 2004

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Page 1

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002s:\*
- 7: geneseqn2003as:\*
- 8: geneseqn2003bs:\*
- 9: geneseqn2003cs:\*
- 10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2842	100.0	2842	3	AAC86411 Wheat sta
2	2788	98.1	2807	3	AAC86435 Wheat sta
3	2474.8	87.1	2939	3	AAC86433 Wheat sta
4	2474.8	87.1	2939	3	AAC86410 Wheat sta
5	2392.2	84.2	2826	2	AAV01528 Wheat gra
6	2175.8	75.6	2920	6	ABK88112 CDNA enco
7	2141.2	75.3	2946	6	ABK88115 CDNA enco
8	2138.4	75.2	2950	6	ABK88113 CDNA enco
9	2137.4	75.2	2951	6	ABK88114 CDNA enco
10	1828.4	64.3	2107	3	AAC86412 Wheat sta
11	1828.4	64.3	2107	3	AAC86434 Wheat sta
12	1297.2	45.6	2607	7	ACC70869 Rice star
13	1294.8	45.6	2607	7	ACC70868 Rice star
14	1246	43.8	2248	3	AAZ50651 Corn star
15	1245.2	43.8	1798	3	AAZ50647 Corn star
16	1245.2	43.8	2019	3	AAZ50646 Corn star
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18	1233.2	43.4	2865	7	ABX09333 Zea may
19	1104.6	38.9	2007	2	AAV29754 DNA encod
20	1104.6	38.9	2007	2	AAV70959 DNA encod
21	1104.6	38.9	2085	2	AAV67286 Soluble s
22	1104.6	38.9	2085	2	AAV66833 Zea may
23	1098	38.6	1724	6	ABX01621 Rice star

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25	1049	36.9	2480	7	ABX09934 DNA encod
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31	806.6	28.4	2418	6	ABSS2841 Typha lat
32	747.2	26.3	5928	7	ACC70867 Rice star
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35	354.4	12.5	5058	6	ABA96385 Wheat car
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#### ALIGNMENTS

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XX  
XX  
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XX  
XX  
XX Wheat starch synthase II coding sequence SEQ ID NO: 3.  
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XX Wheat, starch synthase, SSII; SSIII; starch content; starch synthesis;  
XX food product; adhesive; ss.  
XX  
XX  
XX Triticum aestivum.  
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XX WO200066745-A1.  
XX  
XX 09-NOV-2000.  
XX  
XX 28-APR-2000; 2000MO-AU000385.  
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XX 29-APR-1999; 99AU-0000052.  
XX  
XX (GSTR ) COMMONWEALTH SCI & IND RES ORG.  
XX (GCOO-) GOODMAN FIELDER LTD.  
XX (LINA-) GRP LIMAAGRAIN PACIFIC PTY LTD.  
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XX Morell M, Li Z, Rahman S, Appels R;  
XX WPI; 2000-647602/62.  
XX P-PSDB; AAB37567.  
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XX Nucleic acid molecules encoding wheat starch synthase (WST)-I and WST-II,  
XX useful in modifying plant starch content and/or composition.  
XX  
XX Claim 1; Page 155-158; 21pp; English.  
XX  
XX The present invention relates to novel protein and coding sequences from  
XX wheat. The proteins are wheat starch synthases, designated SSII and  
XX SSIII. These can be used in the modification of plant starch content or  
XX composition, and to screen plants to identify mutations which affect  
XX starch content and composition. The starch can then be used in food  
XX products, such as flour, and in films, coatings, adhesives, building  
XX materials and packaging materials  
XX  
XX Sequence 2842 BP; 561 A; 851 C; 919 G; 511 T; 0 U; 0 Other;

Query Match 100.0%; Score 2842; DB 3; Length 2842;  
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 QY 781 ACCTGAACGTAAGAGAGTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840  
 Db 781 ACCTGAACGTAAGAGAGTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840  
 QY 841 GCGCGCTCGAGCG 900  
 Db 841 GCGCGCTCGAGCG 900  
 QY 901 CGAGAGCG 960  
 Db 901 CGAGAGCG 960  
 QY 961 TGAACATCAACGAACCATGATTCGCGAGCTTTGCGAGGAGAGACGTCATGAACGTCGT 1020  
 Db 961 TGAACATCAACGAACCATGATTCGCGAGCTTTGCGAGGAGAGACGTCATGAACGTCGT 1020

QY 1021 CGTCGTGGCTGCTGAATGTTCTCCCTGCTGCAAAACAGGTGCTTGGAGATGTTGCCGG 1080  
 Db 1021 CGTCGTGGCTGCTGAATGTTCTCCCTGCTGCAAAACAGGTGCTTGGAGATGTTGCCGG 1080  
 QY 1081 TGCCTTGGCCGAAGCTTGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140  
 Db 1081 TGCCTTGGCCGAAGCTTGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140  
 QY 1141 TGGGAGCTATGAGAGAGCTACGATGTCGAGTCCGAAATATCTACAGGCTGTGAGCA 1200  
 Db 1141 TGGGAGCTATGAGAGAGCTACGATGTCGAGTCCGAAATATCTACAGGCTGTGAGCA 1200  
 QY 1201 GGAATGAGAGTGAATTTTCCATGCTTATATGCAAGAGTGAATTTGTTGTTGATGGA 1260  
 Db 1201 GGAATGAGAGTGAATTTTCCATGCTTATATGCAAGAGTGAATTTGTTGTTGATGGA 1260  
 QY 1261 CGCTCTCTCTTCGAGCAACCGCGAGAGACATTTATGCGGCGCGAGAGACAGAAATAT 1320  
 Db 1261 CGCTCTCTCTTCGAGCAACCGCGAGAGACATTTATGCGGCGCGAGAGACAGAAATAT 1320  
 QY 1321 GAAAGGATGATTTTGTTCGCAAGGCGCGTGTGAGAGTTCCTTGGCAGCTTCATAGGG 1380  
 Db 1321 GAAAGGATGATTTTGTTCGCAAGGCGCGTGTGAGAGTTCCTTGGCAGCTTCATAGGG 1380  
 QY 1381 CGGTGTCCCTTATGAGGAGTGAATCTGTGTTTATGCAATGATGTCACACGCGCACT 1440  
 Db 1381 CGGTGTCCCTTATGAGGAGTGAATCTGTGTTTATGCAATGATGTCACACGCGCACT 1440  
 QY 1441 CCGTGTCTGTATGTAAGCATATTAACAGGAGCAATGTTGATGATGATGATGATGATG 1500  
 Db 1441 CCGTGTCTGTATGTAAGCATATTAACAGGAGCAATGTTGATGATGATGATGATGATG 1500  
 QY 1501 CATTAAGTATCAATACATTCGCGCACAGGCGCGTGTGATGATGATGATGATGATG 1560  
 Db 1501 CATTAAGTATCAATACATTCGCGCACAGGCGCGTGTGATGATGATGATGATGATG 1560  
 QY 1561 CACGAGTGTCTGAGGACCTACCTGAGAACCTTCAAGCTGTACGACCCGCGAGTGTGA 1620  
 Db 1561 CACGAGTGTCTGAGGACCTACCTGAGAACCTTCAAGCTGTACGACCCGCGAGTGTGA 1620  
 QY 1621 GACGCGCAACTACTTTCG 1680  
 Db 1621 GACGCGCAACTACTTTCG 1680  
 QY 1681 CGGATACCTGTGGAGCTCAAGAGCGGTGAGAGGCGCGTGGGCGCTTCAACGACATCAG 1740  
 Db 1681 CGGATACCTGTGGAGCTCAAGAGCGGTGAGAGGCGCGTGGGCGCTTCAACGACATCAG 1740  
 QY 1741 GAGAGAGCTGAGAGAGCGCGCGCATCTGCAACGCGATGAGCAATGAGTGTGAAGCC 1800  
 Db 1741 GAGAGAGCTGAGAGAGCGCGCGCATCTGCAACGCGATGAGCAATGAGTGTGAAGCC 1800  
 QY 1801 GAGAGTGAAGCTGAGAGAGCGCGCGCATCTGCAACGCGATGAGCAATGAGTGTGAAG 1860  
 Db 1801 GAGAGTGAAGCTGAGAGAGCGCGCGCATCTGCAACGCGATGAGCAATGAGTGTGAAG 1860  
 QY 1861 CTCGCGCAAGGCGAGTGTGAGAGAGCGCGCGCATCTGCAACGCGATGAGCAATGAGT 1920  
 Db 1861 CTCGCGCAAGGCGAGTGTGAGAGAGCGCGCGCATCTGCAACGCGATGAGCAATGAGT 1920  
 QY 1921 GAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1980  
 Db 1921 GAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1980  
 QY 1981 GCGGAGCGCGCTGCGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2040  
 Db 1981 GCGGAGCGCGCTGCGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2040  
 QY 2041 CGGCGCAAGCTTGAAGAGCATGTGTCGCGCACTTGAAGCGGAGACCAAGAGTGTGCG 2100  
 Db 2041 CGGCGCAAGCTTGAAGAGCATGTGTCGCGCACTTGAAGCGGAGACCAAGAGTGTGCG 2100  
 QY 2101 CGGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2160

[illegible]

XX	29-APR-1999;     99AU-0000052.
PA	(CSIR ) COMMONWEALTH SCI & IND RES ORG.
PA	(GOOD-) GOODMAN FRIEDER LTD
PA	(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX	
P1	Morell M, Li Z, Rahman S, Appels R;
XX	
DR	WPI: 2000-647602/62.
XX	
PT	Nucleic acid molecules encoding wheat starch synthase (WST)-I and WST-II,
PT	useful in modifying plant starch content and/or composition.
XX	
PS	Disclosure, Fig 2, 21pp: English.
CC	
CC	The present invention relates to novel protein and coding sequences from
CC	wheat. The proteins are wheat starch synthases, designated SSII and
CC	SSIII. These can be used in the modification of plant starch content or
CC	composition, and to screen plants to identify mutations which affect
CC	starch content and composition. The starch can then be used in food
CC	products, such as flour, and in films, coatings, adhesives, building
CC	materials and packaging materials
SQ	
SQ	Sequence 2807 BP; 549 A; 844 C; 907 G; 507 T; 0 U; 0 Other;
	Query Match                98.1% Score 2788; DB 3; Length 2807;
	Best Local Similarity    100.0%; Pred. No. 0;
	Matches 2788; Conservative      0; Mismatches    0; Indels    0; Gaps    0;
OY	1 GCTGCACCAACTCGTCGTCTGCGCGCGTCTGGGCGGAGAACCAACCGCGATCGTACC
DB	1 GCTGCCACAACCTTCGCTCTGCGCGCGCTCTCTGGCGGAGAGCAACCGCGATCGTACC
OY	61 ATGCCCCGCCCCGATTCGCGCGCGCGCGCATGTGTTGCGCGTGCGTCCGCGCTCTT
DB	61 ATGCCCCGCCCCGATTCGCGCGCGCGCGCATGTGTTGCGCGTGCGTCCGCGCTCTT
OY	121 CCTCGCGCTCGCTCGCTCTCCCGCGAGATCAAGCAGCGCGGCGAGAGTAGCGCGCC
DB	121 CCGCGCGCTCGCTCGCTCTCCCGCGAGATCAAGCAGCGCGGCGAGAGTAGCGCGCC
OY	181 GCCAACCACGCGCGGGGCGCGGAGGCTGCACTGGCGCGCTGGCGCGCACGCGCGC
DB	181 GCCAACCACGCGCGGGGCGCGGAGGCTGCACTGGCGCGCTGGCGCGCACGCGCGC
OY	241 TCGCAGCAGAGTGTTGCGCGCGCGCGCGCGCGCGCGCGGGAAGAAGACGCGAGGTCAGACAGCA
DB	241 TCGCAGCAGAGTGTTGCGCGCGCGCGCGCGCGCGCGGGAAGAAGACGCGAGGTCAGACAGCA
OY	301 CGCGCGGTCGCGGAGGACGCGCGCGCGCGACGCGCGGTCGCGCGCGCGCGACCAAGTTCGCGGA
DB	301 CGCGCGGTCGCGGAGGACGCGCGCGCGCGACGCGCGGTCGCGCGCGCGCGACCAAGTTCGCGGA
OY	361 GCGAGAGATTCCTGTAAGAGCTTCGATTCGAGACGCCGCGGAAGTTCGCGCGCGCGACCT
DB	361 GCGAGAGATTCCTGTAAGAGCTTCGATTCGAGACGCCGCGGAAGTTCGCGCGCGCGACCT
OY	421 GCGGAGAGATTCCTGTAAGAGCTTCGATTCGAGACGCCGCGGAAGTTCGCGCGCGCGACCT
DB	421 GCGGAGAGATTCCTGTAAGAGCTTCGATTCGAGACGCCGCGGAAGTTCGCGCGCGCGACCT
OY	481 TGAGAAACAATTACCCG
DB	481 TGAGAAACAATTACCCG
OY	541 AGCGCGCGCCATTCGTCGACCCGAGACAGATTCAGTGAACGCTGAACCAAAAGCTAA
DB	541 AGCGCGCGCCATTCGTCGACCCGAGACAGATTCAGTGAACGCTGAACCAAAAGCTAA
OY	601 CGTGCCTTCGCGCGCGCGCGAGACATATGCGCGAGTTCGCGCGCGCGCGCGCGCGCGCGCG
DB	601 CGTGCCTTCGCGCGCGCGCGAGAGATATGCGCGAGTTCGCGCGCGCGCGCGCGCGCGCGCG
OY	660 CGTGCCTTCGCGCGCGCGCGAGAGATATGCGCGAGTTCGCGCGCGCGCGCGCGCGCGCGCG
DB	660 CGTGCCTTCGCGCGCGCGCGAGAGATATGCGCGAGTTCGCGCGCGCGCGCGCGCGCGCGCG

QY	661	TTTCATTCATGACGACAAAGCCGCGAGTCCGTTGTCCACGCGAAGCCGCGCGTGGTC	720
Db	661	TTTCATTCATGACGACAAAGCCGCGAGTCCGTTGTCCACGCGAAGCCGCGCGTGGTC	720
QY	721	CGGCTCAAAATTCGTGCTCGGCTCTGTGCTCCGAGGCTGACATTTGACAGGATTTGA	780
Db	721	CGGCTCAAAATTCGTGCTCGGCTCTGTGCTCCGAGGCTGACATTTGACAGGATTTGA	780
QY	781	ACCTGAATCGAAGAGGGATGCGGTCACTGTCGAAGAGCTCCAAACCBAAGGCTCTTC	840
Db	781	ACCTGAATCGAAGAGGGATGCGGTCACTGTCGAAGAGCTCCAAACCBAAGGCTCTTC	840
QY	841	GCCGCTTCGACGCCCCGCTGTACAAABAACCTTTGGGACTTCAGAAATACATTTGGCT	900
Db	841	GCCGCTTCGACGCCCCGCTGTACAAABAAGCCTTTGGGACTTCAGAAATACATTTGGCT	900
QY	901	CGAGAGCCCGGTGAGAGCCAGAGATGATGAGTGGGCTTTGAGATGATGCGGCTCTT	960
Db	901	CGAGAGCCCGGTGAGAGCCAGAGATGATGAGTGGGCTTTGAGATGATGCGGCTCTT	960
QY	961	TGAACATCACAGAACCATGATTTCCGACCTTTGGCAGGGAGAAAGCTCATGAACTGGT	1020
Db	961	TGAACATCACAGAACCATGATTTCCGACCTTTGGCAGGGAGAAAGCTCATGAACTGGT	1020
QY	1021	CGACGAGCGCTGGAATGTTCTCCCTGATSCAAACAGAGTGTCTTGAGATGTTGCCG	1080
Db	1021	CGACGAGCGCTGGAATGTTCTCCCTGATSCAAACAGAGTGTCTTGAGATGTTGCCG	1080
QY	1081	TGCTTTGCCCAAGGCTTTGSCGAAGAGAGCACTCGTATTATGTTGTGTACCAAGTA	1140
Db	1081	TGCTTTGCCCAAGGCTTTGSCGAAGAGAGCACTCGTATTATGTTGTGTACCAAGTA	1140
QY	1141	TGGGAGTATAGAGGAAGCTACGATGTCGAGATCCGAAATACATAAGGCTGTGGACA	1200
Db	1141	TGGGAGTATAGAGGAAGCTACGATGTCGAGATCCGAAATACATAAGGCTGTGGACA	1200
QY	1201	GGATATGGAAGTGAATTTATTCATGCTTAAATGATGATGATGATTTGTGTTCAATGA	1260
Db	1201	GGATATGGAAGTGAATTTATTCATGCTTAAATGATGATGATGATTTGTGTTCAATGA	1260
QY	1261	CGCTCTCTCTTCGGAACCGCCAGGAAGACATTTAGGGGAGCAGACAGGAATTAAT	1320
Db	1261	CGCTCTCTCTTCGGAACCGCCAGGAAGACATTTAGGGGAGCAGACAGGAATTAAT	1320
QY	1321	GAAAGCATGATTTTGTGTTGTCGAAGGCGCGCTGTGAGGTTCTTTGACAGTTCCATGCG	1380
Db	1321	GAAAGCATGATTTTGTGTTGTCGAAGGCGCGCTGTGAGGTTCTTTGACAGTTCCATGCG	1380
QY	1381	CGGTGTCCCTTAATGGGATGGAATCTGTGTATTATAGCAATGATTTGGACACGCGACT	1440
Db	1381	CGGTGTCCCTTAATGGGATGGAATCTGTGTATTATAGCAATGATTTGGACACGCGACT	1440
QY	1441	CCTGCGTGTATCTGAAAGCATTTACAGGACCATGTTTGAATGACATCACTCGCTC	1500
Db	1441	CCTGCGTGTATCTGAAAGCATTTACAGGACCATGTTTGAATGACATCACTCGCTC	1500
QY	1501	CATTATGTTGATACATAATCATGCGGACACAGGCGCGGACCAATGATGAAATCCCGTT	1560
Db	1501	CATTATGTTGATACATAATCATGCGGACACAGGCGCGGACCAATGATGAAATCCCGTT	1560
QY	1561	CACGAGTGTGCTGAGCACTACCTGGAACAATTGACATGTACACACCCCGTGGTGTGA	1620
Db	1561	CACGAGTGTGCTGAGCACTACCTGGAACAATTGACATGTACACACCCCGTGGTGTGA	1620
QY	1621	GCAGCGCACTAATTCGCGCGCGGCTGAAGATGCGGACCAAGTGTGCTGTGTGAGACCC	1680
Db	1621	GCAGCGCACTAATTCGCGCGCGGCTGAAGATGCGGACCAAGTGTGCTGTGTGAGACCC	1680
QY	1681	CGGATACCTGTGGAGCTCAACAGGTGAGAGGCGGCTGTGAGGCTTACGACATATACG	1740
Db	1681	CGGATACCTGTGGAGCTCAACAGGTGAGAGGCGGCTGTGAGGCTTACGACATATACG	1740
QY	1741	GCAGAACTGATGAGAACCCGCGCATCTCAACGCGCATTCAGCAATGAGAGTGAACCC	1800

Db	1741	GCAGAACGACTGGAGAACCCCGGGGATGGTCAACGGGCAATCGAACATGGAGTGGAA	1800
QY	1801	CGAGGTGGACGTCCACTTCGAACTCGGAGGGCTTACCAAATTCCTCCCTGGGGACGCTGG	1860
Db	1801	CGAGGTGGACGTCCACTTCGAACTCGGAGGGCTTACCAAATTCCTCCCTGGGGACGCTGG	1860
QY	1861	CTCCGGCAAGCGGCACTGGCAAGAGGACCTGGCAGCGCGAGCTGGGCTTCAGAGTCCGCG	1920
Db	1861	CTCCGGCAAGCGGCACTGGCAAGAGGACCTGGCAGCGCGAGCTGGGCTTCAGAGTCCGCG	1920
QY	1921	CGAGGTGCCGTCTCGGCTTCATCGGCCGCTCGAGCGGGCAAGAGGGCTGGAGTCAAT	1980
Db	1921	CGAGGTGCCGTCTCGGCTTCATCGGCCGCTCGAGCGGGCAAGAGGGCTGGAGTCAAT	1980
QY	1981	CGCGGACCGCATAGCCCTGGATCGTAGGACGAGGACGTCAGCTGGTCACTGGGCA	2040
Db	1981	CGCGGACCGCATAGCCCTGGATCGTAGGACGAGGACGTCAGCTGGTCACTGGGCA	2040
QY	2041	CGCGCACGACCTGGAGAGCATGCTGGGCACTTCGAGCGGGACACCAAGCAAGGTGG	2100
Db	2041	CGCGCACGACCTGGAGAGCATGCTGGGCACTTCGAGCGGGACACCAAGCAAGGTGG	2100
QY	2101	CGGGTGGGTGGGGTTCTCCGTGGGCTGGGCGCACCGGATCACGGCGGGGCGCGACGCGCT	2160
Db	2101	CGGGTGGGTGGGGTTCTCCGTGGGCTGGGCGCACCGGATCACGGCGGGGCGCGACGCGCT	2160
QY	2161	CGTCATGCGCTCCCGGTTGAGCGCGGTGGAGCCAGCTTTACGCCATGGCTTAACG	2220
Db	2161	CGTCATGCGCTCCCGGTTGAGCGCGGTGGAGCCAGCTTTACGCCATGGCTTAACG	2220
QY	2221	CACCGTCCCGCTGTGTGACGCGCTCGGCGGGGTGAAGGACACCGTCCCGCTTTACAGCC	2280
Db	2221	CACCGTCCCGCTGTGTGACGCGCTCGGCGGGGTGAAGGACACCGTCCCGCTTTACAGCC	2280
QY	2281	CTTCAACCACTCCGCGCTCGGGTGGAGCTTTCAGCCGCGCGGAGCGCACAAAGTGAATGA	2340
Db	2281	CTTCAACCACTCCGCGCTCGGGTGGAGCTTTCAGCCGCGCGGAGCGCACAAAGTGAATGA	2340
QY	2341	GGCGCTCGGACCTGCTCGGACCTTACCGGAGCTTACAGAGAAAGCTGGAGGGGCGCTCCA	2400
Db	2341	GGCGCTCGGACCTGCTCGGACCTTACCGGAGCTTACAGAGAAAGCTGGAGGGGCGCTCCA	2400
QY	2401	GGAGCGCGGAGTGTGCGGAGACTTCAGCTGGAGCAATGCGCGAAAGCTTTACGAGAGAGCT	2460
Db	2401	GGAGCGCGGAGTGTGCGGAGACTTCAGCTGGAGCAATGCGCGAAAGCTTTACGAGAGAGCT	2460
QY	2461	CGTCTTCAAGGCGCAAGTACCAAGTGGTGAACGCTTACGCCGCTTCAGCCCCGAGTGG	2520
Db	2461	CGTCTTCAAGGCGCAAGTACCAAGTGGTGAACGCTTACGCCGCTTCAGCCCCGAGTGG	2520
QY	2521	CGTGCATGCAATGAGAGGGTGAAGTTCGAGATGCGCGCGCGAGGAACTGTGCATCTTCTC	2580
Db	2521	CGTGCATGCAATGAGAGGGTGAAGTTCGAGATGCGCGCGCGAGGAACTGTGCATCTTCTC	2580
QY	2581	GATGGAGCGCGCGCATCCGCGAGGTGACATGATAGAGGTGTGTGTGTGTAGAGCGC	2640
Db	2581	GATGGAGCGCGCGCATCCGCGAGGTGACATGATAGAGGTGTGTGTGTGTAGAGCGC	2640
QY	2641	TGATTCGATTCGATCTGCTGCTGAGCAGTGAAGCGGACGTAAGGAACGCTCTCTG	2700
Db	2641	TGATTCGATTCGATCTGCTGCTGAGCAGTGAAGCGGACGTAAGGAACGCTCTCTG	2700
QY	2701	TTGCAAGTAATGGGAATGTTTCAACTGGTATTTGATTTGCTATGTTGTAATGCGTTA	2760
Db	2701	TTGCAAGTAATGGGAATGTTTCAACTGGTATTTGATTTGCTATGTTGTAATGCGTTA	2760
QY	2761	TTACAAATGTGTACTATTCTTGTGA 2788	
Db	2761	TTACAAATGTGTACTATTCTTGTGA 2788	

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AAC86433
ID AAC86433 standard; cDNA; 2939 BP.
XX
XX AAC86433;
AC
XX 01-MAR-2001 (first entry)
DT
XX
XX Wheat starch synthase clone WSSIIA cDNA.
DE
XX Wheat starch synthase; SSII; SSIII; starch content; starch synthesis;
KW food product; adhesive; ss.
XX
XX Triticum aestivum.
OS
XX WO200066745-A1.
PN
XX
XX
XX
XX 09-NOV-2000.
XX
XX
XX 28-APR-2000; 2000WO-AU000385.
XX
XX
XX 29-APR-1999; 99AU-00000052.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX (GOOD-) GOODMAN FIELDER LTD.
XX (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX
XX
XX Morell M, Li Z, Rahman S, Appels R;
XX
XX WPI, 2000-647602/62.
XX
XX Nucleic acid molecules encoding wheat starch synthase (WST)-I and WST-II,
XX PT useful in modifying plant starch content and/or composition.
XX
XX Disclosure; Fig 2; 21pp; English.
XX
XX
XX The present invention relates to novel protein and coding sequences from
XX CC wheat. The proteins are wheat starch synthases, designated SSII and
XX CC SSIII. These can be used in the modification of plant starch content or
XX CC composition, and to screen plants to identify mutations which affect
XX CC starch content and composition. The starch can then be used in food
XX CC products, such as flour, and in films, coatings, adhesives, building
XX CC materials and packaging materials
XX
XX
XX Sequence 2939 BP; 580 A; 892 C; 946 G; 521 T; 0 U; 0 Other;
SQ
Query Match 87.1%; Score 2474.8; DB 3; Length 2939;
Best Local Similarity 94.8%; Pred. No. 0;
Matches 2621; Conservative 0; Mismatches 117; Indels 26; Gaps 5
QY 2 CTGCGACACACTCTCGGCTGCGCGCGCTGCGGCGGAGAGACCAACCGCGCATGTATACCA 61
DB 89 CTGCGACACACTCTCGGCTGCGCGCGCTGCGGCGGAGAGACCAACCGCGCATGTATACGA 148
QY 62 TCGCCGCCGCCGATCCCGGCGCGCGCATGTCTGCGCGGTCTCGCTCCCGGCTCCTTC 1211
DB 149 TCACCCACACCCCGATCCCGGCGCGCGCATGTCTGCGCGGTCTCGCTCCCGGCTCCTTC 2081
QY 122 CTGCGCGCTGCGCTCTCGCGCTCCCGCGGAGATCAAGCAGCGGAGGAGGTGAGCGCGCG 1811
DB 209 CTGCGCGCTGCGCTCTCGCGCTCCCGCGGAGATCAAGCAGGAGGAGGAGCGCTCG 2681
QY 182 CCAACCCAGCGCGCGCGCGCGAGGCTGCACTGAGCTGCGCGCTGCGCGCGCGCGAGCGGCT 2411
DB 269 CCAACCCAGCGCGCGCGCGGTGCGAGGTTGCACTGAGCTGCGCGCGCGCGAGCGGCT 3281
QY 242 CGAGCAGGAGGTGCGCGCGCGCGCGCGCGCGCGAGAGAGACGCGAGGATCGAGCGAGC 3011
DB 329 CGGAGCGGAGCGGTGCGCGCGCGCGCGCGCGCGGAGAGAGAGCGGAGGAT---GAGGAC 3881
QY 302 GCGCGGTCTCGGAGGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 3611
DB 386 GCGCGCGCGCGGAGGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 4451

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QY	362	CGAGAGGATATCCCGTCAAGACGCTTCATCGCAGACGCGCGGAAGGTGCGCGCGGACACG	421
Db	446	CGAGAGGATATCCCGTCAAGAGCGCTCATTCGCGACGCGCGGAAGGTGCGCGCGCTCCCG	505
QY	422	CCGCGACCGAGGACAGACGCGCGCGCTTCAACGAGATATGACGCGACGCGCGGTGAGACGT	481
Db	506	CCGCGACCGAGGACAGGAGGACGCGCGCTTCGCGAGATGAGACGCGACGCGGTGAGACGT	565
QY	482	GAGAACAAATCTACCGCGCGCGCGCGCGGACGCAAGAACAGCGCGGTGCGCGCGACCGCA	541
Db	566	GAGAACAAATCTACCGCGCGCGCGCGCGGACGCTAAAGACAGCGCGGTGCGCGCGACCGCA	625
QY	542	CGCGCGCGCGCATCCGTGACCCAGAACAGAGTACCAATGACCGGTGAGAACAAAGCTAAC	601
Db	626	CGCGCGCGCGCATCCGTGACCCAGAACAGAGTACCGGTGAGAACAAAGCTAAC	685
QY	602	GTCGCGCTCGCGCGCGAGACATAGCCGAGGTGCGGTCCGGATTCCGAGCTACATT	661
Db	686	GTCGCGCTCGCGCGCGAGACATAGCCGAGGTGCGGTCCGGATTCCGAGCTACATT	745
QY	662	TCCATCAAGTACAGAGCGCGCGAGTCCGTGTCCACGCCAGAACCGCGCGGTGTC	721
Db	746	TCCATCAAGTACAGAGCGCGAGTCCGTGTCCACGCCAGAACCGCGCGGTGTC	805
QY	722	GCGTCAAAATTCGTGCTCGGCTTCTGCTCCAGGCTGACATGACACGAGTGTGA	781
Db	806	GCGTCAAAATTCGTGCTCGGCTTCTGCTCCAGGCTGACATGACACGAGTGTGA	865
QY	782	CTGTAAGTGAAGAGGAGGAGCGGTATCGTGAAGAACTCCAAACCCAAAGGCTTTTCG	841
Db	866	CTGTAAGTGAAGAGGAGGAGCGGTATCGTGAAGAACTCCAAACCCAAAGGCTTTTCG	925
QY	842	CCGCGCTGAGGCCCCCGCTGTACAAGAACCTTTGGACTTCAAGAAATACATTGCTTC	901
Db	926	CCGCGCTGAGGCCCCCGCTGTACAAGAACCTTTGGACTTCAAGAAATACATTGCTTC	985
QY	902	GAGAGACCGGTGAGAGGCCAAGAGATGATGGCTGGGCTGTTGACATGATGCGGCTCCTTT	961
Db	986	GAGAGACCGGTGAGAGGCCAAGAGATGATGGCTGGGCTGTTGACATGATGCGGCTCCTTT	1045
QY	962	GAACATCACACGAACCATGATTCGACCTTTGGACAGGAGAACTCATGACGTGCTC	1021
Db	1046	GAACATCACACGAACCATGATTCGAGGCTTTGGACAGGAGAACTCATGACGTGCTC	1105
QY	1022	GTCGTGCTGCTGTAATGTTCTCCCTGTGTGCAAAACAGTGTCTTGAAGATGTTCCGGT	1081
Db	1106	GTCGTGCTGCTGTAATGTTCTCCCTGTGTGCAAAACAGTGTCTTGAAGATGTTCCGGT	1165
QY	1082	GCTTGTCCCAAGGCTTTGGCAGAGAGACATGTTGATGTTGTGTGTTACCAAGTAT	1141
Db	1166	GCTTGTCCCAAGGCTTTGGCAGAGAGACATGTTGATGTTGTGTGTTACCAAGTAT	1225
QY	1142	GCGGACTATGAGAAAGCCATGATTCGAGTCCGAAATATCTACAGGCTGTGACAG	1201
Db	1226	GCGGACTATGAGAAAGCCATGATTCGAGTCCGAAATATCTACAGGCTGTGACAG	1285
QY	1202	GATATGGAAGGAATTAATTTCCATGCTATATTCGATGAGAGTTGATTTGTGTTCATTGAC	1261
Db	1286	GATATGGAAGGAATTAATTTCCATGCTATATTCGATGAGAGTTGATTTGTGTTCATTGAC	1345
QY	1262	GCTCCTCTTTCGACACCGCCAGGAACAATTATGGGGGACGACACAGAAATTAATG	1321
Db	1346	GCTCCTCTTTCGACACCGCCAGGAACAATTATGGGGGACGACACAGAAATTAATG	1405
QY	1322	AAGCGAGATTAATTTGTTTCGACAGGCGGTGTGAGTTCCTTGGCACGTTTCATGCGGC	1381
Db	1406	AAGCGAGATTAATTTGTTTCGACAGGCGGTGTGAGTTCCTTGGCACGTTTCATGCGGC	1465
QY	1382	GGTGTCCCTTATGGGATGGAATCTGTGTTTATTGCAAAATGATTTGACACGCACTC	1441
Db	1466	GGTGTCCCTTATGGGATGGAATCTGTGTTTATTGCAAAATGATTTGACACGCACTC	1525
QY	1442	CTGCGGTATCTGAAAGCAATTTACAGGACCATGTTGATGTCAGTACCTGCTCC	1501

Db 1526 CTGCTCTTATCTGAAAGCATTTACAGAGACATGTTTATGAGTACACTCGATCC 1585  
 Qy 1502 ATTATGATGATATACATTCGGGACACAGGCGCGTGGCCGATGATATATATCCCGTTC 1561  
 Db 1586 ATTATGATGATATACATTCGGGACACAGGCGCGTGGCCGATGATATATATCCCGTTC 1645  
 Qy 1562 ACCGAGTGGCTGAGCACTACCTGGAACATTGACATGACACCCCGTGGTGGTGA 1621  
 Db 1646 ACCGAGTGGCTGAGCACTACCTGGAACATTGACATGACACCCCGTGGTGGTGA 1705  
 Qy 1622 CACGCAACTACTTTCGCGCGCGGCTGAGATGGCGGACAGGTTGTCTGGTGGTGGC 1681  
 Db 1706 CACGCAACTACTTTCGCGCGCGGCTGAGATGGCGGACAGGTTGTCTGGTGGTGGC 1765  
 Qy 1682 GGGTACCTGTGGAGCTCAAGACGATGAGGCGGCTGGGGCTTGACGACATCATACG 1741  
 Db 1766 GGGTACCTGTGGAGCTCAAGACGATGAGGCGGCTGGGGCTTGACGACATCATACG 1825  
 Qy 1742 CAGAACGACTGGAAGACCGCGGCGATGTCACAGGATGCAATGAGTGGAAACCC 1801  
 Db 1826 CAGAACGACTGGAAGACCGCGGCGATGTCACAGGATGCAATGAGTGGAAACCC 1885  
 Qy 1802 GAGGTGAGACCTGCAAGTGGAGGAGGCTTACACCACTTCTCCCTGGGAGCGTGGAC 1861  
 Db 1886 GAGGTGAGACCTGCAAGTGGAGGAGGCTTACACCACTTCTCCCTGGGAGCGTGGAC 1945  
 Qy 1862 TCCGCAAGCGGCACTGCAAGAGAGCCCTGACGCGAGCTGGGCTTGAGTCCGCGC 1921  
 Db 1946 TCCGCAAGCGGCACTGCAAGAGAGCCCTGACGCGAGCTGGGCTTGAGTCCGCGC 2005  
 Qy 1922 GAGTGGCTGCTGCTGCTTATGAGGCGCGCTGAGCGGAGAGAGGCGTGGAGTATC 1981  
 Db 2006 GAGTGGCTGCTGCTGCTTATGAGGCGCGCTGAGCGGAGAGAGGCGTGGAGTATC 2065  
 Qy 1982 GCGGACGCTGCTGCTGCTGAGGCGGAGCGTGGAGTATGAGTGGAGCGGCT 2041  
 Db 2066 GCGGACGCTGCTGCTGCTGAGGCGGAGCGTGGAGTATGAGTGGAGCGGCT 2125  
 Qy 2042 CGCCACGACTGAGAGAGATCTCGGAGCTTCAAGGCGGAGCGACGACAAAGTGGC 2101  
 Db 2126 CGCCACGACTGAGAGAGATCTCGGAGCTTCAAGGCGGAGCGACGACAAAGTGGC 2185  
 Qy 2102 GGGTGGTGGGTTCTCCGCTGCTGCGACCGGATCAAGGCGGCGCGGCGCTC 2161  
 Db 2186 GGGTGGTGGGTTCTCCGCTGCTGCGACCGGATCAAGGCGGCGCGGCGCTC 2245  
 Qy 2162 CTGATGCTCTCCGCTGCTGAGGCGGCTGCGGTTTGAACCAAGCTTTCAGCTAGCG 2221  
 Db 2246 CTGATGCTCTCCGCTGCTGAGGCGGCTGCGGTTTGAACCAAGCTTTCAGCTAGCG 2305  
 Qy 2222 ACCGTCCTCCGCTGCTGAGGCGGCTGCGGTTTGAACCAAGCTTTCAGCTAGCG 2281  
 Db 2306 ACCGTCCTCCGCTGCTGAGGCGGCTGCGGTTTGAACCAAGCTTTCAGCTAGCG 2365  
 Qy 2282 TTCAACCACTCCGCTGCTGAGGCGGCTGCGGTTTGAACCAAGCTTTCAGCTAGCG 2341  
 Db 2366 TTCAACCACTCCGCTGCTGAGGCGGCTGCGGTTTGAACCAAGCTTTCAGCTAGCG 2425  
 Qy 2342 GGGCTCGGAGCACTGCTCGGACCTACCGGAGCTTCAAGAGAGGCTGAGGCGCTCCAG 2401  
 Db 2426 GGGCTCGGAGCACTGCTCGGACCTACCGGAGCTTCAAGAGAGGCTGAGGCGCTCCAG 2485  
 Qy 2402 GAGCGCGCATGCTCGGAGCTTCAAGTGGAGCATTCGCGCAACTTTCAGAGAGCTC 2461  
 Db 2486 GAGCGCGCATGCTCGGAGCTTCAAGTGGAGCATTCGCGCAACTTTCAGAGAGCTC 2545  
 Qy 2462 CTGCTTAAAGGCAAGTACAGTGGTGAAGCTAGCTAGCGCTTCAAGCGCCCGCATGC 2521  
 Db 2546 CTGCTTAAAGGCAAGTACAGTGGTGAAGCTAGCTAGCGCTTCAAGCGCCCGCATGC 2605  
 Qy 2522 GTGATGATGAGAGGAGTGAAGTGGCATTTGGCGCCGAGGAAAGTGCATCTTTCG 2581

Db 2606 G---TGATGACAGATGGAATTGGCCATTTGGCCACGACGAGAAAGTGGCAT----- 2653  
 Qy 2582 ATGGAGCGCGGAGATCCGCGAGTGAGTGAATGAGAGTGTGTGGTTGAGACGCT 2641  
 Db 2654 ---GAGCGCGGAGATCCGCGAGTGAAGTGAATGAGAGTGTGTGGTTGAGACGCT 2708  
 Qy 2642 GATTCGATCTCATCTGCTGCTGCGTACGAGTGAAGGCGACGTAAGGAGCGCTCTGT 2701  
 Db 2709 GATTC-----CGATCTGCTGCGTACGAGTGAAGGCGACGTAAGGAGCGCTCTGT 2762  
 Qy 2702 TGACGATATAGGAGATGTTGCACTTGTGATTTGATTGCTATGTTATGCGTTAT 2761  
 Db 2763 TACAGTATATGAGAAATGTTGTTACTTGTATGTTATGTTATGTTATGTTATG 2822  
 Qy 2762 TACA 2765  
 Db 2823 TACA 2826  
 RESULT 4  
 AAC86410  
 ID AAC86410 standard; cDNA; 2939 BP.  
 AAC86410;  
 01-MAR-2001 (first entry)  
 DE Wheat starch synthase II coding sequence SEQ ID NO: 1.  
 XX Wheat; starch synthase; SSII; SSIII; starch content; starch synthesis;  
 KW food product; adhesive; ss.  
 OS Triticum aestivum.  
 PN WO20066745-A1.  
 XX 09-NOV-2000.  
 PD 28-APR-2000; 2000WO-AU000385.  
 XX 29-APR-1999; 99AU-00000052.  
 PR (CSTR) COMMONWEALTH SCI & IND RES ORG.  
 PA (GOOD-) GOODMAN FIELDER LTD.  
 PA (LIMA-) GRP LIMARAIN PACIFIC PTY LTD.  
 PI Morell M, Li Z, Rahman S, Appels R;  
 XX WPI: 2000-647602/62.  
 DR P-PSDB; AAB37566.  
 PT Nucleic acid molecules encoding wheat starch synthase (WST-I and WST-II,  
 XX useful in modifying plant starch content and/or composition.  
 PS Claim 1; Page 149-152; 211pp; English.  
 CC The present invention relates to novel protein and coding sequences from  
 CC wheat. The proteins are wheat starch synthases, designated SSII and  
 CC SSIII. These can be used in the modification of plant starch content or  
 CC composition, and to screen plants to identify mutations which affect  
 CC starch content and composition. The starch can then be used in food  
 CC products, such as flour, and in films, coatings, adhesives, building  
 CC materials and packaging materials  
 XX  
 SQ Sequence 2939 BP; 580 A; 892 C; 946 G; 521 T; 0 U; 0 Other;  
 Query Match 87.1%; Score 2474.8; DB 3; Length 2939;  
 Best Local Similarity 94.8%; Pred. No. 0; Mismatches 117; Indels 26; Gaps 5;  
 Matches 2621; Conservative 0;  
 Qy 2 CTGCAACCACTCCGCTGCTGCGGCTGCTGAGGCGGAGACCAACCGCGCATCTGTA 61  
 Db 89 CTGCAACCACTCCGCTGCTGCGGCTGCTGAGGCGGAGACCAACCGCGCATCTGTA 148



QY 62 TCGCCGCGCCCGATCCCGGCGCGCATGTGCTGCGCGTCCGCTCCGCGCTTC 121  
 Db 149 TCACCCACCCCGATCCCGGCGCGCATGTGCTGCGCGTCCGCTCCGCGCTTC 208  
 QY 122 CTCGCGCTCGCCCTCCGCGCTCCCGGAGATCAACGAGCGGCGAGGTTGAGCGCGC 181  
 Db 209 CTCGCGCTCGCGCTCCGCGCTCCCGGAGATCAACGAGCGGCGAGGTTGAGCGCGC 268  
 QY 182 CCAACCCACGCGCGGCGCGAGCTGCACTGCGCGCGCTGCGCGCGCGCGAGCT 241  
 Db 269 CCAACCCACGCGCGGCGCGAGCTGCACTGCGCGCGCTGCGCGCGCGCGAGCT 328  
 QY 242 CGGAGCGAGGTTGCGCGCGCGCGCGCGCGCGGAGAGAGAGCGCGGTTGAGAGAGC 301  
 Db 329 CGGAGCGAGGTTGCGCGCGCGCGCGCGCGCGGAGAGAGAGCGCGGTTGAGAGAGC 385  
 QY 302 GCGCGCTCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 361  
 Db 386 GCGCGCGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 445  
 QY 362 CGGAGGATCCCGTCAAGAGCTGCACTGCGAGCGCGCGGAGAGGTTGCGCGAGC 421  
 Db 446 CGGAGGATCCCGTCAAGAGCTGCACTGCGAGCGCGCGGAGAGGTTGCGCGAGC 505  
 QY 422 CGGAGCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 481  
 Db 506 CGGAGCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 565  
 QY 482 GAGAGCAATCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 541  
 Db 566 GAGAGCAATCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 625  
 QY 542 CGGCGCGCGCGATCGGTGAGCCGAGACAGAGTACGAGTACGCGCGGTGAGAGCT 601  
 Db 626 CGGCGCGCGCGATCGGTGAGCCGAGACAGAGTACGAGTACGCGCGGTGAGAGCT 685  
 QY 602 GTGCGCTCGCGCGCGAGCGAGCATAGCGAGGTCGTGCGCGCTCCGAGTTCGAGT 661  
 Db 686 GTGCGCTCGCGCGCGAGCGAGCATAGCGAGGTCGTGCGCGCTCCGAGTTCGAGT 745  
 QY 662 TCATCTAGTACAGAGCGCGCGAGTCCGTGTCGCGAGCGAGAGCGCGCGCGTGC 721  
 Db 746 TCATCTAGTACAGAGCGCGCGAGTCCGTGTCGCGAGCGAGAGCGCGCGCGTGC 805  
 QY 722 GCGTCAATTCGAGTCTCGCGCTTCGCTCCGAGCTGAGCATGAGCGATGTGA 781  
 Db 806 GCGTCAATTCGAGTCTCGCGCTTCGCTCCGAGCTGAGCATGAGCGATGTGA 865  
 QY 782 CTTAATCTGAAGAGGTCGTGATCTGCGAGAGAGTCCAAACCCAAAGGCTCTTGG 841  
 Db 866 CTTAATCTGAAGAGGTCGTGATCTGCGAGAGAGTCCAAACCCAAAGGCTCTTGG 925  
 QY 842 CCGCTCGAGCGCGCGCTGTAACAAGAGCTTGGAGTTCAGAAATACATTTGCTTC 901  
 Db 926 CCGCTCGAGCGCGCGCTGTAACAAGAGCTTGGAGTTCAGAAATACATTTGCTTC 985  
 QY 902 GAGAGCGCGTGAAGCGAGAGATGATGCTGCGCTTTCGAGATGATGCGGCTCTT 961  
 Db 986 GAGAGCGCGTGAAGCGAGAGATGATGCTGCGCTTTCGAGATGATGCGGCTCTT 1045  
 QY 962 GAGATCAACAGAGATGATTCGAGCTTGGAGCGAGAGAGTCAAGAGCTGATG 1021  
 Db 1046 GAGATCAACAGAGATGATTCGAGCTTGGAGCGAGAGAGTCAAGAGCTGATG 1105  
 QY 1022 GTGCTGCTGCTGAATGTTCTCCGTGCGAGAGAGTGTTCGAGATGTTGCGGCT 1081  
 Db 1106 GTGCTGCTGCTGAATGTTCTCCGTGCGAGAGAGTGTTCGAGATGTTGCGGCT 1165  
 QY 1082 GCTTTCAGAGGCTTTCGAGAGAGAGAGATCATGCTGTTATGTTGTGATCAAGGAT 1141  
 Db 1166 GCTTTCAGAGGCTTTCGAGAGAGAGAGATCATGCTGTTATGTTGTGATCAAGGAT 1225

QY 1142 GGGATCTATGAGAGAGCTTACGATGTGAGAGTCCGAGAAATACATCAAGGCTGAGAG 1201  
 Db 1226 GGGATCTATGAGAGAGCTTACGATGTGAGAGTCCGAGAAATACATCAAGGCTGAGAG 1285  
 QY 1202 GATATGAGAGATTTATTTCACTGCTTATGATGATGAGATGATTTGTTTCAATTGAC 1261  
 Db 1286 GATATGAGAGATTTATTTCACTGCTTATGATGATGAGATGATTTGTTTCAATTGAC 1345  
 QY 1262 GCTTCTCTTTCGAGACCGCGAGAGAGATTTATGAGGCGAGAGAGAGAGATTTATG 1321  
 Db 1346 GCTTCTCTTTCGAGACCGCGAGAGAGATTTATGAGGCGAGAGAGAGAGATTTATG 1405  
 QY 1322 AAGGATGATTTTGTCTGAGAGCGCGCTGTCGAGAGTTCCTTGGACGTTTCATGCGG 1381  
 Db 1406 AAGGATGATTTTGTCTGAGAGCGCGCTGTCGAGAGTTCATGAGACGTTTCATGCGG 1465  
 QY 1382 GGTGTCCCTTATGAGGAGTGAATCTGTGTTATTTGCAATGATTTGGACACGAGCTC 1441  
 Db 1466 GGTGTCCCTTATGAGGAGTGAATCTGTGTTATTTGCAATGATTTGGACACGAGCTC 1525  
 QY 1442 CTGCTGTCTATGAGAGCATATTACAGGAGACATGTTGATGAGTACATCGTTC 1501  
 Db 1526 CTGCTGTCTATGAGAGCATATTACAGGAGACATGTTGATGAGTACATCGTTC 1585  
 QY 1502 ATTATGATATCAATACATGCGAGACAGAGCGCGTGGCCGAGTATGATTTCCGTT 1561  
 Db 1586 ATTATGATATCAATACATGCGAGAGCGCGTGGCCGAGTATGATTTCCGTT 1645  
 QY 1562 ACCGAGTGGCTGAGAGCTACTGAGAGCATTCGAGATGATGAGAGAGAGAGAGAG 1621  
 Db 1646 ACCGAGTGGCTGAGAGCTACTGAGAGCATTCGAGATGATGAGAGAGAGAGAGAG 1705  
 QY 1622 CACGCGCATCTTCGCGCGCGCGCTGAGAGTGGCGAGACAGTGTGTTGTTGAGAGCC 1681  
 Db 1706 CACGCGCATCTTCGCGCGCGCGCTGAGAGTGGCGAGACAGTGTGTTGTTGAGAGCC 1765  
 QY 1682 GGTATCCGTGAGAGCTCAAGAGGTTGAGAGGCGCGCTGAGAGATGATGAGAG 1741  
 Db 1766 GGTATCCGTGAGAGCTCAAGAGGTTGAGAGGCGCGCTGAGAGATGATGAGAG 1825  
 QY 1742 CAGAGCGATGAGAGAGCGCGCGAGTCTGACAGCGAGTCAACATGAGTGAACCC 1801  
 Db 1826 CAGAGCGATGAGAGAGCGCGCGAGTCTGACAGCGAGTCAACATGAGTGAACCC 1885  
 QY 1802 GAGTGAAGCTTCACCTCAATGAGAGGCTGACACCACTTCTCCGAGAGAGCTGAG 1861  
 Db 1886 GAGTGAAGCTTCACCTCAATGAGAGGCTGACACCACTTCTCCGAGAGAGCTGAG 1945  
 QY 1862 TCCGAGAGCGAGTGAAGAGAGCGCTGAGAGCGAGTGAAGTGAAGTCCGCGC 1921  
 Db 1946 TCCGAGAGCGAGTGAAGAGAGCGCTGAGAGCGAGTGAAGTGAAGTCCGCGC 2005  
 QY 1922 GAGTGGCTGCTGCTGCTTATGAGCGCGCTGAGAGCGAGAGGCGTGAATCATC 1981  
 Db 2006 GAGTGGCTGCTGCTGCTTATGAGCGCGCTGAGAGCGAGAGGCGTGAATCATC 2065  
 QY 1982 GCGAGCGCATGCGCTGATGAGAGCGAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 2041  
 Db 2066 GCGAGCGCATGCGCTGATGAGAGCGAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 2125  
 QY 2042 CCGCAGAGCTGAGAGAGCTGCGAGCTTCAGAGCGAGAGACACAGAGTGAAG 2101  
 Db 2126 CCGCAGAGCTGAGAGAGCTGCGAGCTTCAGAGCGAGAGACACAGAGTGAAG 2185  
 QY 2102 GGTGAGGTTGAGGTTTCCGTGCGCTGAGAGCGAGATCAAGAGGCGAGAGCGGCTC 2161  
 Db 2186 GGTGAGGTTGAGGTTTCCGTGCGCTGAGAGCGAGATCAAGAGGCGAGAGCGGCTC 2245  
 QY 2162 CTATGAGCTTCGAGGTTGAGAGCGGCTGAGAGCTTGAACAGCTTATGAGCATGAGCT 2221  
 Db 2246 CTATGAGCTTCGAGGTTGAGAGCGGCTGAGAGCTTGAACAGCTTATGAGCATGAGCT 2305  
 QY 2222 ACCGTCCCGTGTGAGAGCGCGTGGCGGAGTGAAGAGACAGGTCGCGCGTGAACCC 2281

Db		2306	ACCGTCCCGTCGTGCATGTCGGTGCTGAAGGACAACCGTGCCTTGAACCCC	2365		
Qy		2282	TTCAACCACTTCGCCGCTTCGGGTGGACGTTTGCACC GGCCGACCAAGCTGATGACG	2341		
Db		2366	TTCAAACCACTCCGGGCTCGGGTGAAGTCATTGACCCGAGAGGCGCAGAAGCTGATGAG	2425		
Qy		2342	GCGCTCGGAGCACTGCTCCGCACTTACCGGACTACAGAGAGAGAGCTGAGGAGCTTCAG	2401		
Db		2426	GCCTTCGGGACCTGCTCCTCCGACCTAACGGAGACTAACAAGAGAGACTGAGGAGCTTCAG	2485		
Qy		2402	GAGCGCGGCACTGTGGCAGGACTTTCAGCTGGGAGGATGCCCGCAAGCTCTACGAGAGCTC	2461		
Db		2486	GAGCGCGGCACTGTGGCAGGACTTTCAGCTGGGAGGATGCCCGCAAGCTCTACGAGAGCTC	2545		
Qy		2462	CTCCTCAAGGCCAAGTACCAAGTAGTGTAACGCTAGCTGTAGCCGCTCACGCCCGCATGC	2521		
Db		2546	CTCCTCAAGGCCAAGTACCAAGTAGTGTAACGCTAGCTGTAGCCGCTCACGCCCGCATGC	2605		
Qy		2522	GTGCATGCAATAGAGAGGCTGTAACCTGGCATGGCCCGCAGAGAGCTGATCCTTCCTG	2581		
Db		2606	G-----TGATATACAGATGATGATAATTGCGCATTCGCAACGAGAGAGATGCCAT-----	2653		
Qy		2582	ATGGAGAGCGCGGCAATCCGCGAGGTGCAGTGAACATGAGAGGTGTGTGTGTTGAGACGCT	2641		
Db		2654	---GAGAGCGCGGCAATCCGCGAGTACAGTGAACAT--GAGGTGTGTGTGTTGAGACGCT	2708		
Qy		2642	GATTCGCATCTCCAGATCTGCTGCCGTAGCAGAGTAGAGGAGGAGCGTACCGCTCTGT	2701		
Db		2709	GATTC-----GATCTGCTCCGTAGCAGATGAGCGGAGTAGAGGAGGAGCGCTCTGT	2762		
Qy		2702	TGCAGGATATATAGGAAATGTGTCAACTTGTAATGTAGTTGTCTATGTGTATGGCTAT	2761		
Db		2763	TACAGGATATATAGGAAATGTGTGTAACTTGTAATGTATTTGTATGTGTGTGATTAAT	2822		
Qy		2762	TACA 2765			
Db		2823	TACA 2826			
<hr/>						
RESULT 5						
ID	AAV01528					
	AAV01528 standard; cDNA to mRNA; 2826 BP.					
XX	AAV01528;					
AC						
DT	27-AUG-2003 (revised)					
DT	21-MAY-1998 (first entry)					
DE	Wheat granule-bound starch synthase cDNA clone pTAS1.					
KW	Starch synthase; wheat; transgenic plant; ss.					
OS	Triticum aestivum.					
XX						
FT	Key	Location/Qualifiers				
FT	CDS	162..2561				
FT		/*tag= a				
PB	MO9745545-Al.					
PD	04-DEC-1997.					
PF	28-MAY-1997;	97WO-EP002793.				
PR	29-MAY-1996;	96DE-01021588.				
PR	11-SEP-1996;	96DE-01036917.				
PA	(AGRE ) HOECHST-SCHERING AGREVO GMBH.					
PI	Block M, Loefer H, Luetticke S, Walter L, Froberg C, Kossmann J,					
DR	WPI; 1998-032652/03.					

Query Match	Best Local Similarity	Matches 2613;	Conservative	84.2%;	Score 2392.2;	DB 2;	Length 2826;	
				93.8%;	Pred. No. 0;	Mismatches 108;	Indels 66;	Gaps 9
XX	P-PSDB; AAM23938.							
XX	Nucleic acid encoding starch synthase enzymes from wheat - for transgenic plants that produce modified forms of starch, useful e.g. in foods, or for production of packaging materials and disposable goods.							
XX	Claim 1; Page 54-58; 71pp; English.							
CC	This full-length cDNA clone, designated pTAS1, codes for a granule bound starch synthase (see AAM23638) of summer wheat (cv. Floradep). It was isolated from a phase cDNA library of 21-day-old wheat callus. It is screening with antibodies raised against 3 peptides (see AAM2393-41) representing strongly conserved regions of starch synthases in other organisms. A second, partial clone (see AAM2397), coding for wheat							
CC	solubled starch synthase (see AAM2397) is also claimed. These isolated nucleic acids can be inserted into vectors for production of transgenic plants, particularly starch-producing plants, specifically wheat. Use of the isolated nucleic acids, or of antisense sequences, allows starch metabolism to be regulated in transgenic plants. Overexpression may result in improved crop yield, while modification of starch in plants may eliminate the need for subsequent chemical/physical modification. Plants with altered levels of the various isoforms of starch synthase will produce starch of different chain length, amylose/amylopectin ratio, degree of branching, phosphate content, gelatinisation behaviour, granule size and shape, viscosity etc. The starch produced by such plants is useful particularly in foods or to produce packaging materials or disposable goods, as well as in any other known use of starch. (Updated on 27-AUG-2003 to correct OS field.)							
CC	Sequence 2826 BP; 567 A; 864 C; 891 G; 504 T; 0 U; 0 Other;							
XX								
CC	Query Match							
CC	Best Local Similarity							
CC	Matches 2613;							
CC	Conservative							
CC	84.2%;							
CC	Score 2392.2;							
CC	DB 2;							
CC	Length 2826;							
CC	93.8%;							
CC	Pred. No. 0;							
CC	Mismatches 108;							
CC	Indels 66;							
CC	Gaps 9							
CC	2 CTGCACCACTCTCCGCTTGGCGCGCTCTTGGCGGAGAGACCAACCCGCGCATGTATCCA 61							
CC	89 CTGCACCACTCTCCGCTTGGCGCGCTCTTGGCGGAGAGACCAACCCGCGCATGTATCCA 145							
CC	62 TTGCGCGCGCGCATCCCGCGCGCGCGCATGTCTGGCGGCGGTCTCCGCGGTCTTCC 121							
CC	146 TCTCCGCGCGCAT-----CAATGTCTGGCGGTCTCCGCGCATCTTCC 194							
CC	122 CTGCGCGTCTCCGCTCTCCGCGCGCGCGCATGTATCAGCAAGCGGAGGATGAGCGCGCG 181							
CC	195 CTGCGCGTCTCCGCTCTCCGCGCGCGCGCATGTATCAGCAAGCGGAGGATGAGCGCGCG 254							
CC	182 CACACCCACGCGCGCGCGCGCGCGCGCATGTATGAGCGCGCGGTGGCGCGCGCGCGCGCT 241							
CC	255 CACACCCACGCGCGCGCGCGCGCGCGCATGTATGAGCGCGCGGTGGCGCGCGCGCGCGCT 314							
CC	242 CCGGACGAGGTGTGGCTCG 301							
CC	315 CCGGACGAGGTGTGGCTCG 374							
CC	302 GCGCGCGTCTCCG 361							
CC	375 GCGCGGTCTCCG 434							
CC	362 CCGGACGAGGTGTGGCTCG 421							
CC	435 CCGGACGAGGTGTGGCTCG 494							
CC	422 CCGGACGAGGTGTGGCTCG 481							
CC	495 CCGGACGAGGTGTGGCTCG 554							
CC	482 GAGGACCAATCTTACCGGCG 541							
CC	555 GAGGACCAATCTTACCGGCG 614							
CC	542 CG 601							

Db 615 CGCGCGCCCATCCGTGACCCAGAAACAGAGCACCGGTGAACGGTGAACAAAGCTAAC 674  
Qy 602 GTGGCCTCGCGCGCGAGACATAGCCAGAGTGTGTGCTCCGGATTCGGAGCTACATT 661  
Db 675 GTGGCCTCGCGCGCGAGACATAGCCAGAGTGTGTGCTCCGGATTCGGAGCTACATT 734  
Qy 662 TCCATCAGTGAACAAGCGCGGAGTCCGTTGTCCAGCCGAGAAAGCCGCGCGTGTCC 721  
Db 735 TCCATCAGCGACAAGCGCGGAGTCCGTTGTCCAGCTGAAGAACGCGCGTGTCC 794  
Qy 722 GGGCTCAATTTCTGTGTCTCGGCTTCTGCTCCAGGTGACATTTGAACGGATTTTGA 781  
Db 795 GGGCTCAATTTCTGTGTCTCGGCTTCTGCTCCAGCTGAAGAACGCGCGTGTCC 854  
Qy 782 CCTGAATGAAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 841  
Db 855 CAAAGACTGAAGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 914  
Qy 842 CCGCTCGAGCGCGCGCTGTACAAAGACCTTTGGACCTTCAAGAAATTCATTGGCTTC 901  
Db 915 CCGCTCGAGCGCGCGCTGTACAAAGACCTTTGGACCTTCAAGAAATTCATTGGCTTC 974  
Qy 902 GAGAGCGCGGTGAGGCGCAAGAGATGATGATGATGATGATGATGATGATGATGATGATG 961  
Db 975 GAGAGCGCGGTGAGGCGCAAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1034  
Qy 962 GAACATCAACCAAAACATGATTCGAGACTTTGGACGGGAGAACTCATGAACGTGTCTC 1021  
Db 1035 GAACATCAACCAAAACATGATTCGAGACTTTGGACGGGAGAACTCATGAACGTGTCTC 1094  
Qy 1022 GTGCGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1081  
Db 1095 GTGCGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1154  
Qy 1082 GCTTGTCCCAAGGCTTTGGCGAAGAGAGACATGATGATGATGATGATGATGATGATGATG 1141  
Db 1155 GCTTGTCCCAAGGCTTTGGCGAAGAGAGACATGATGATGATGATGATGATGATGATGATG 1214  
Qy 1142 GGGGACTGAGAGAGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1201  
Db 1215 GGGGACTGAGAGAGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1274  
Qy 1202 GATATGAAGTGAATTAATTCATGCTTAATGATGATGATGATGATGATGATGATGATG 1261  
Db 1275 GATATGAAGTGAATTAATTCATGCTTAATGATGATGATGATGATGATGATGATGATG 1334  
Qy 1262 GCTCTCTCTTCCGACACCGCGAGAGAACTTTATGGGGGACAGAAAGAAATTAAG 1321  
Db 1335 GCTCTCTCTTCCGACACCGCGAGAGAACTTTATGGGGGACAGAAAGAAATTAAG 1394  
Qy 1322 AAGGCAATGATTTGTTCTGCAAGGCGCTGTGAGGTTCTTGGACAAGTTCCATGCGGC 1381  
Db 1395 AAGGCAATGATTTGTTCTGCAAGGCGCTGTGAGGTTCTTGGACAAGTTCCATGCGGC 1454  
Qy 1382 GATGCTCTTATGGGAGTGAATGTGTGTTTATGCAATGATGATGATGATGATGATGATG 1441  
Db 1455 GATGCTCTTATGGGAGTGAATGTGTGTTTATGCAATGATGATGATGATGATGATGATG 1514  
Qy 1442 CTGCGCTGTCTTATGGAAGCATATTAACGAGACATGATGATGATGATGATGATGATGATG 1501  
Db 1515 CTGCGCTGTCTTATGGAAGCATATTAACGAGACATGATGATGATGATGATGATGATGATG 1574  
Qy 1502 ATTATGATGATCATTAACATGCGGACAGAGGCGCTGTGAGCTGATGATGATGATGATG 1561  
Db 1575 ATTATGATGATCATTAACATGCGGACAGAGGCGCTGTGAGCTGATGATGATGATGATG 1634  
Qy 1562 ACCGAGTTGGCTGAGACATGATGATGATGATGATGATGATGATGATGATGATGATG 1621  
Db 1635 ACCGAGTTGGCTGAGACATGATGATGATGATGATGATGATGATGATGATGATGATG 1694  
Qy 1622 CAGCGCAACTACTTGGCGCGCGCTGAGAGATGAGCGGACAGATGATGATGATGATGATG 1681  
Db 1695 CAGCGCAACTACTTGGCGCGCGCTGAGAGATGAGCGGACAGATGATGATGATGATGATG 1754

Qy 1682 GGGTACCTGTGGAGCTCAAGACCGTGAAGAGCGGCTGGGGGCTTCAACATCATACCG 1741  
Db 1755 GGGTACCTGTGGAGCTGAAGACCGTGAAGAGCGGCTGGGGGCTTCAACATCATACCG 1814  
Qy 1742 CAGAACTGATGAAAGACCCCGGAGATGATCAACCGCATTCACAAATGAGATGAAACCC 1801  
Db 1815 CAGAACTGATGAAAGACCCCGGAGATGATCAACCGCATTCACAAATGAGATGAAACCC 1874  
Qy 1802 GAGGTGAGATGCACTCAATGCGGAGATGATGATGATGATGATGATGATGATGATGATG 1861  
Db 1875 GAGGTGAGATGCACTCAATGCGGAGATGATGATGATGATGATGATGATGATGATGATG 1934  
Qy 1862 TCCGCAAGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1921  
Db 1935 TCCGCAAGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1994  
Qy 1922 GACGTGCGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1981  
Db 1995 GACGTGCGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2054  
Qy 1982 GCGAGCGCATGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2041  
Db 2055 GCGAGCGCATGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2114  
Qy 2042 CCGCAAGACCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2101  
Db 2115 CCGCAAGACCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2174  
Qy 2102 GGGTGGTGGGTTCTCGGTGCGCTGCGGACCGGATCAAGCGGGGCGCGGCTG 2161  
Db 2175 GGGTGGTGGGTTCTCGGTGCGCTGCGGACCGGATCAAGCGGGGCGCGGCTG 2234  
Qy 2162 CTCATGCGCTCCCGGTTGAGACCGCTGCGGTTGAACCAAGCTTTACGGCATGCGG 2221  
Db 2235 CTCATGCGCTCCCGGTTGAGACCGCTGCGGTTGAACCAAGCTTTACGGCATGCGG 2294  
Qy 2222 ACCGTGCCGCTGTGACAGCGCGTGGCGGGTGAAGGACACCGTGCCTGTCACCCC 2281  
Db 2295 ACCGTGCCGCTGTGACAGCGCGTGGCGGGTGAAGGACACCGTGCCTGTCACCCC 2354  
Qy 2282 TTCAACCACTCGGCTCGGTTGAGACCTTCAACCGCGCGGAGGAGCAATGATGATG 2341  
Db 2355 TTCAACCACTCGGCTCGGTTGAGACCTTCAACCGCGCGGAGGAGCAATGATGATG 2414  
Qy 2342 GCGCTCGGCACTGCTCGGCACTACCGGAGCTCAAGAGAGCTGAGGGGCTCCAG 2401  
Db 2415 GCGCTCGGCACTGCTCGGCACTACCGGAGCTCAAGAGAGCTGAGGGGCTCCAG 2474  
Qy 2402 GAGCGGCGATGCGAGAGCTTCACTGCGGAGCATGCGGCAAGCTTCAAGAGAGCT 2461  
Db 2475 GAGCGGCGATGCGAGAGCTTCACTGCGGAGCATGCGGCAAGCTTCAAGAGAGCT 2534  
Qy 2462 CTCCTCAAGGCAAGTCAAGTGTGAAGCGTAGCTGTAGCGCTCCAGCCCGCATG 2521  
Db 2535 CTCCTCAAGGCAAGTCAAGTGTGAAGCGTAGCTGTAGCGCTCCAGCCCGCATG 2594  
Qy 2522 GTGCATGATGAGAGGTGAAGCTGCGATGCGGCTCGGAGAGCTGCGATCTTCTCG 2581  
Db 2595 GTGCATGATGAGAGGTGAAGCTGCGATGCGGCTCGGAGAGCTGCGATCTTCTCG 2640  
Qy 2582 ATGGAGCGCGCGGATGCGGAGGTGAGTGAATGAGAGGTGATGATGATGATGATG 2641  
Db 2641 ATGGAGCGCGCGGATGCGGAGGTGAGTGAATGAGAGGTGATGATGATGATGATGATG 2695  
Qy 2642 GATTCGATCTGATCTGTGCTGAGACAGAGTGAAGCGGACGTAGGAAAGCGCTCTGT 2701  
Db 2696 GATTCGATCTGATCTGTGCTGAGACAGAGTGAAGCGGACGTAGGAAAGCGCTCTGT 2728  
Qy 2702 TCGAGTATATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2761  
Db 2729 TCGAGTATATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2782

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Page 10

QY 2762 TACATGTTGTTACTTATCTGTTAA 2788  
DB 2783 TACATGTTGTTACTTATCTGTTAA 2809

RESULT 6

ABK8112  
ID ABK8112 standard; CDNA; 2920 BP.

ABK8112;

07-OCT-2002 (first entry)

CDNA encoding modified barley starch synthase II (SSII).

Barley; starch synthase II; SSII; high amylose; reduced amylopectin;

food production; swelling volume; gelatinisation temperature;

reduced swelling; reduced viscosity; low crystallinity; instant noodle;

V form starch crystallinity; dietary fibre; instant soup; gene; ss.

Hordeum vulgare.

Location/Qualifiers  
Key 114..252

/tag= a

/product= "SSII"

/note= "Starch synthase II"

/transl\_except= (pos:350..353, aa:Pro)

W0200237955-A1.

16-MAY-2002.

09-NOV-2001; 2001WO-AU001452.

09-NOV-2000; 2000AU-00001370.

09-NOV-2000; 2000AU-00001371.

09-NOV-2000; 2000AU-00001372.

09-NOV-2000; 2000AU-00001373.

(CSIR) COMMONWEALTH SCI & IND RES ORG.

Morell MK, Topping D, Batey IL;

WPI: 2002-557434/59.

P-PSDB; AAU99845.

New barley plant for producing starch with improved characteristics, has

reduced level of SSII activity and is capable of bearing grain.

Claim 140; Fig 9; 107BP; English.

The invention describes a barley plant (I) with a reduced level of starch

synthase II (SSII) activity and capable of bearing grain, where the

starch of the grain has a high amylose content by reason of a reduced

amylopectin content and the grain (II) are useful for food production. (I),

the starch (II) and the grain (II) are useful for food products, in food

processing procedures, and in dietary and food processing applications.

(II) has reduced amylopectin content, and relatively high amylose

content. (II) exhibits a low swelling volume (2.0-3.2). The grain has

relatively high beta-glucan content. (II) has low gelatinisation

temperature, reduced swelling, reduced viscosity and low crystallinity.

The starch also has high levels of lipid exhibiting very high levels of V

form starch crystallinity. The dietary fibre content of the starch is

high. The starch thus provides a prospect of significantly enhancing the

nutritional benefits of foods, where there is a requirement of rapid

preparation, such as instant soups and instant noodles. This sequence

encodes the starch synthase II with reduced activity described in the

invention

Sequence 2920 BP; 585 A; 848 C; 913 G; 574 T; 0 U; 0 Other;

Query Match 76.6%; Score 2175.8; DB 6; Length 2920;  
Best Local Similarity 88.5%; Pred. No. 0;  
Matches 2511; Conservative 0; Mismatches 227; Indels 99; Gaps 10;

QY 46 CCGGCGCATGTTACATGCGCCCGCCGATCCGCGCCCGCCGATGCTGCGCGCTCGC 105  
DB 71 CCGGCGCATGTTACATGCGCCCGCCGATCCGCGCCCGCCGATGCTGCGCGCTCGC 130  
QY 106 GTCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 162  
DB 131 GTCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 190  
QY 163 GCGGAGGCTGAGCG 222  
DB 191 GCGGAGGCTGAGCG 250  
QY 223 GCGGCG 282  
DB 251 GCGGCG 303  
QY 283 GCGGAGGCTGAGCG 342  
DB 304 -----TCGACGACG 352  
QY 343 CCGGCGCATGTTACATGCGCCCGCCGATCCGCGCCCGCCGATGCTGCGCGCTCGC 402  
DB 353 CCGGCGCATGTTACATGCGCCCGCCGATCCGCGCCCGCCGATGCTGCGCGCTCGC 403  
QY 403 AGGTGAGCG 462  
DB 404 AGGTGAGCG 463  
QY 463 CCGGCGCATGTTACATGCGCCCGCCGATCCGCGCCCGCCGATGCTGCGCGCTCGC 522  
DB 464 CCGGCGCATGTTACATGCGCCCGCCGATCCGCGCCCGCCGATGCTGCGCGCTCGC 523  
QY 523 CCGGCG 582  
DB 524 CCGGCG 583  
QY 583 CCGTGAAGGCTGAGCG 642  
DB 584 CCGTGAAGGCTGAGCG 643  
QY 643 GGTATCG 702  
DB 644 GGTATCG 703  
QY 703 GAAAGCG 729  
DB 704 GAAAGCG 763  
QY 730 TTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 789  
DB 764 TTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 823  
QY 790 GAAAGGAGGCTGAGCG 849  
DB 824 GAAAGGAGGCTGAGCG 863  
QY 850 AGCG 909  
DB 864 AGCG 943  
QY 910 CCGGAGGCTGAGCG 969  
DB 944 CCGGAGGCTGAGCG 1003  
QY 970 CCGGAGGCTGAGCG 1029  
DB 1004 CCGGAGGCTGAGCG 1063  
QY 1030 TGTGTAATGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1089

Db 1064 TGCTGAATGTTCTCCCTGGTGCAGAAACAGGTGCTCTTGAGATGTTGCGGGTGTTC 1123  
 Qy 1090 CAAGGCTTTGGGAGAGAGAGACATGCTGTATGTTGATACCAAGGATGGGACATA 1149  
 Db 1124 CAAGGCTTTGGGAGAGAGAGACATGCTGTATGTTGATACCAAGGATGGGACATA 1183  
 Qy 1150 TGAGAGAGCTTACGATGTGAGATCCGAAATACTACAAAGGCTGTGACAGATATGGA 1209  
 Db 1184 TGAGAGAGCTTACGATGTGAGATCCGAAATACTACAAAGGCTGTGACAGATATGGA 1243  
 Qy 1210 AGTGAATATATTCGATGCTTATATGATGAGATGATTTGTTGATATGAGGCTCTCT 1269  
 Db 1244 AGTGAATATATTCGATGCTTATATGATGAGATGATTTGTTGATATGAGGCTCTCT 1303  
 Qy 1270 CTTCGACACCGCCAGAGAGACATTTATGGGGCAGACAGACAGAAATTAAGAGCGCAT 1329  
 Db 1304 CTTCGACACCGCCAGAGAGACATTTATGGGGCAGACAGAGAAATTAAGAGCGCAT 1363  
 Qy 1330 GATTTGTCTTCAGAGGCGCTGTGAGGTTCTTGGACGTTCCATGGGGGGGTCTCC 1389  
 Db 1364 GATTTGTCTTCAGAGGCGCTGTGAGGTTCTTGGACGTTCCATGGGGGGGTCTCC 1423  
 Qy 1390 TTAATGGGATGAGAAATCTGTGTATATGCAATGATGGACACGCGCATCTCTGCTGT 1449  
 Db 1424 TTAATGGGATGAGAAATCTGTGTATATGCAATGATGGACACGCGCATCTCTGCTGT 1483  
 Qy 1450 CTATCTGAAGACATATTTACAGGACCATGTTGATGACGATACCTCGCTCATATGCT 1509  
 Db 1484 CTATCTGAAGACATATTTACAGGACCATGTTGATGACGATACCTCGCTCATATGCT 1543  
 Qy 1510 GATACATACATGCGCGACACGAGGCGGTGGCCAGTGAATGAAATCCGTTACCGAGTT 1569  
 Db 1544 GATACATACATGCGCTACACGAGGCGGTGGCCAGTGAATGAAATCCGTTACCGAGTT 1603  
 Qy 1570 GCGTGAACATCTCTGAGACATTTAGACTGTACGACCCCGTGGTGTGAGACACCCAA 1629  
 Db 1604 GCGTGAACATCTCTGAGACATTTAGACTGTACGACCCCGTGGTGTGAGACACCCAA 1663  
 Qy 1630 CTACTTGGCGCGCGCTGAAAGATGAGGAGCCAGGTTGTGTTGAGACCCCGGATACCT 1689  
 Db 1664 CTACTTGGCGCGCGCTGAAAGATGAGGAGCCAGGTTGTGTTGAGACCCCGGATACCT 1723  
 Qy 1690 GTGGAGGCTCAAGACGCTGAGAGGCGCTGAGGCGCTTACAGACATCATACGGAAGACA 1749  
 Db 1724 GTGGAGGCTCAAGACGCTGAGAGGCGCTGAGGCGCTTACAGACATCATACGGAAGACA 1783  
 Qy 1750 CTGGAAGACCCGCGGACATCTGTCACGCGCATTCGAAATGAGAAACCCCGAGGTGA 1809  
 Db 1784 CTGGAAGACCCGCGGACATCTGTCACGCGCATTCGAAATGAGAAACCCCGAGGTGA 1843  
 Qy 1810 CGTCCACCTCAAGTCTGACGCGCTACACCACTTCTCCCTGGGAGCGCTGACATCCGCA 1869  
 Db 1844 CGTCCACCTCAAGTCTGACGCGCTACACCACTTCTCCCTGGGAGCGCTGACATCCGCA 1903  
 Qy 1870 GCGGAGTGTCAAGAGGCGCTGACGCGGAGACTGGGCTGTGAGGTTCCGCGCCAGCTGCC 1929  
 Db 1904 GCGGAGTGTCAAGAGGCGCTGACGCGGAGACTGGGCTGTGAGGTTCCGCGCGCACTGCC 1963  
 Qy 1930 GCTGCTCGGCTTCAATCGCGCGCTGACGCGGAGAGGCGCTGAGATCATCCGCGAGCG 1989  
 Db 1964 GCTGCTCGGCTTCAATCGCGCGCTGACGCGGAGAGGCGCTGAGATCATCCGCGAGCG 2023  
 Qy 1990 CATGCTCTGAGTGTGAGCTCAGACGTCAGCTGTCTATGCTGGGACACCGCGCCACGA 2049  
 Db 2024 CATGCTCTGAGTGTGAGCTCAGACGTCAGCTGTCTATGCTGGGACACCGCGCCACGA 2083  
 Qy 2050 CCGTGAAGACATGCTGCGGCACTTTCGAGCGGAGACACAGACAAAGTGTCCGCGGTGGT 2109  
 Db 2084 CCGTGAAGACATGCTGCGGCACTTTCGAGCGGAGACACAGACAAAGTGTCCGCGGTGGT 2143  
 Qy 2110 GGGGTTCTCCGCTGCGCTGTGGCGACCGGATCACGCGCGCGCCGACGCGCTCTCATGCC 2169

Db 2144 GGGGTTCTCCGCTGCGCTGTGGCGACCGGATCAACGCGCGCGCCGACGCGCTCTCATGCC 2203  
 Qy 2170 CTCCGCTTTCAGACCGCTGCGGCTTTGAACAGCTTTACGCAATGCGCTTACGCGACCGTCCC 2229  
 Db 2204 CTCCGCTTTCAGACCGCTGCGGCTTTGAACAGCTTTACGCAATGCGCTTACGCGACCGTCCC 2263  
 Qy 2230 CGTGTGACAGCGCGCTGCGCGGAGTGAAGGACACCGTCCCGCTTCAACCA 2289  
 Db 2264 CGTGTGACAGCGCGCTGCGCGGAGTGAAGGATACCGTCCCGCTTCAACCA 2323  
 Qy 2290 CTCCGCGCTCGGCTGAGAGCTTTCGACCGCGCCAGGCGCACAGCTGATCAGAGCGCTGCG 2349  
 Db 2324 CTCCGCGCTCGGCTGAGAGCTTTCGACCGCGCCAGGCGCACAGCTGATCAGAGCGCTGCG 2383  
 Qy 2350 GCATGCTCTCCGCACTTACCGGAGCTTACAGAGAGAGTGAAGGCGCTCCAGAGACGCGG 2409  
 Db 2384 GCATGCTCTCCGCACTTACCGGAGCTTACAGAGAGAGTGAAGGCGCTCCAGAGACGCGG 2443  
 Qy 2410 CATGTGCAAGACCTTACGCTGAGAGCAATGCGCCAGCTCTACAGAGACGCTCTCTCAA 2469  
 Db 2444 CATGTGCAAGACCTTACGCTGAGAGCAATGCGCCAGCTCTACAGAGACGCTCTCTCAA 2503  
 Qy 2470 GCGCAAGTACAGTGTGAGAACGCTAGCTGTGAGCGCTCCAGCGCCGATGCGGCAATGC 2529  
 Db 2504 GCGCAAGTACAGTGTGAGAACGCTAGCTGTGAGCGCGCTCCAGCGCCGATGCGGCAATGC 2555  
 Qy 2530 ATGAGAGGCTGAACCTGCGCATT-----GCGCCGACAGAAAGTGC 2572  
 Db 2556 ATGAGAGGATGAATATGCGATTTGCGCACTTTCAGATTTGGCGACAGAAAGTGC 2615  
 Qy 2573 TCTTTCTGATGAGAGCGCGCATTCGCGAGGTCAGTGAATGAGAGTGTGTGTGT 2632  
 Db 2616 TCTTTCTGATGAGAGCGCGCATTCGCGAGGTCAGTGAATGAGAGTGTGTGTGT 2675  
 Qy 2633 TGAGAGCGTGAATTCGATCTGATCGGCTCGTACAGAGTGAAGCGGACGTAAGGAGC 2692  
 Db 2676 TGAGAGCGTGAATTCGATCTGATCGGCTCGTACAGAGTGAAGCGGACGTAAGGAGC 2735  
 Qy 2693 GCTCTTGTTCAGATATGAGGAGTGTGCACTTGTGATTTGCTATGTTGT 2752  
 Db 2726 TTTTTCGAGGAGGATATGAGGAGTGTGCACTTGTGATTTGCTATGTTGT 2792  
 Qy 2753 ATGCTTTTCA-----ATGTTTACTTATTTT-----GTAAAGTGGAGGCAAGGCG 2804  
 Db 2793 GTGCAATTAATCAGCGGTTGTTGCTTATTTCTGATGATGCGAGGCGCAAGGCG 2852  
 Qy 2805 GAAAGCTAGCTCACATG 2821  
 Db 2853 GAAAGCTAGCTCACATG 2869

RESULT 7  
 ABK8115  
 ID ABK8115 standard; cDNA; 2946 BP.  
 XX  
 XX ABK8115;  
 DE 07-OCT-2002 (first entry)  
 XX  
 XX cDNA encoding barley line 292 starch synthase II (SSI1).  
 KM Barley; starch synthase II; SSI1; high amylose; reduced amylopectin;  
 KM food production; swelling volume; gelatinisation temperature;  
 KM reduced swelling; reduced viscosity; low crystallinity; instant noodle;  
 KM V form starch crystallinity; dietary fibre; instant soup; gene; ss;  
 KM line 292.  
 XX  
 XX Hordeum vulgare.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH 107.2548  
 FT CDS  
 FT /tag= a  
 FT /product= "SSI1"





Db 1477 TGGAAATGATGGCACACGGCACTCTGCTGTCTATCTGAAGCATATTATTCAGGACCA 1536  
 Oy 1477 TGGTTTGAATGACATTAACCTCGCTCCATTATGGTATACATTAACATCGGACACAGGCGCG 1536  
 Db 1537 TGGTTTGAATGACATTAACCTCGCTCCATTATGGTATACATTAACATCGGACACAGGCGCG 1596  
 Oy 1537 TGGCCCGATGATGAATATTCCTGTTACCGAGTTGGCTGAGCACTTCTGAAACACTTTCAG 1596  
 Db 1597 TGGCCCGATGATGAATATTCCTGTTACCGAGTTGGCTGAGCACTTCTGAAACACTTTCAG 1656  
 Oy 1597 ACTGTATGACCCCGTGGGTGTGTGACGACGCACTTCTTCCGCGGCTGAAAGTGGC 1656  
 Db 1657 ACTGTATGACCCCGTGGGTGTGTGACGACGCACTTCTTCCGCGGCTGAAAGTGGC 1716  
 Oy 1657 GGAACAGGTGTGTGTGTGAGCCCGGATCTGTGGAGCTCAAGACGGTGGAGGGCGG 1716  
 Db 1717 GGAACAGGTGTGTGTGTGAGCCCGGATCTGTGGAGCTCAAGACGGTGGAGGGCGG 1776  
 Oy 1717 CTGGGGCTTTCACGACATCACTACGAGCAAGACGCTGGAAGACCGGGGATCTGGAACGG 1836  
 Db 1777 CATCGACATGAGAGTGAACCCCGAGTGAAGTCACTCAAGTGGACGGCTACAC 1836  
 Oy 1837 CATCGACATGAGAGTGAACCCCGAGTGAAGTCACTCAAGTGGACGGCTACAC 1896  
 Db 1897 CAATCTCTCCCTGAAGACGCTGACCTCGGCAAGCGGCACTGCAAGAGGCTCTGACGG 1956  
 Oy 1897 CGAGCTGGGCTTGAAGTCCGCGGACGAGTGGCTGTGGCTTATCGGCGGCTGGA 1956  
 Db 1957 CGAGCTGGGCTTGAAGTCCGCGGACGAGTGGCTGTGGCTTATCGGCGGCTGGA 2016  
 Oy 1957 CGGCGAGAGGCGCTGAGATCATCGCGAGCGCATCTGATCGTGAAGCAGACGT 2076  
 Db 2017 GCACTGTGTATCTGTGGGACCCGCGGCAAGCTTGAAGACATGCTGGGACATTTCA 2076  
 Oy 2077 GCACTGTGTATGTGTGGGACCGGCGGCAAGCTTGAAGACATGCTGAAGACTTTCA 2136  
 Db 2077 GCGGAGACACACACACAGAGTCCGCGGATGGGATTCCTCGTGGCTGGCGCACCG 2136  
 Oy 2137 GCGGAGACACACACAGAGTCCGCGGATGGGATTCCTCGTGGCTGGCGCACCG 2196  
 Db 2137 GATCACGGCGGCGCGGACGCGCTCTCATGCTCCGCTTCAGGCTGGCGGCTGAA 2256  
 Oy 2197 GATCACGGCGGCGCGGACGCGCTCTCATGCTCCGCTTCAGGCTGGCGGCTGAA 2256  
 Db 2197 CCAGCTTACGCACTGAGCTTACGCGGACCGTCCCGTGTGTGACGCGCTTCGCGGATGAG 2256  
 Oy 2257 CCACTCTACGCGATGGCTTACGCGGACCGTCCCGTGTGTGACGCGCTTCGCGGATGAG 2316  
 Db 2257 GGAACACGCTGCGCGCTTCAACCACTTCCGCGGCTTCGCGGATGAG 2376  
 Oy 2317 GGAACACGCTGCGCGCTTCAACCACTTCCGCGGCTTCGCGGATGAG 2376  
 Db 2317 GCGCGAGGCGGACAGAGTGTGAGGCGCTGGGCACTGCTCCGCACTTACCGGAGCTA 2376  
 Oy 2377 GCGCGAGGCGGACAGAGTGTGAGGCGCTGGGCACTGCTCCGCACTTACCGGAGCTA 2436  
 Db 2437 CAAGGAGAGCTGAGAGGCGCTTCAGAGACGCGGATGTGAGAGCTTCAAGCTGGAGCA 2496  
 Oy 2437 TGGCGGCAAGCTTACGAGAGCTTCTCAAGGCGGCAAGTACAGTGGTGAACGCTAGC 2496  
 Db 2497 TGGCGGCAAGCTTACGAGAGCTTCTCAAGGCGGCAAGTACAGTGGTGAACGCTAGC 2552  
 Oy 2497 TGGTACCGCTTCAGCGCCCGCATGCGTGCATGATGAGAGGCTGAACTGCGCAT 2552

Db 2553 TGTACCCGGTCCAGCCCGCATGCG---TGATGAGAGATGAAATGCGATTGCGC 2608  
 Oy 2553 -----GCGCCCGAGAGACGTGCAATCTTCTGATGGAGCGCGGCAATCC 2599  
 Db 2609 ACTTGAGATTTGGCGGACCGGAGAGCTGCGCTCTTCTGATGAGAACGCGGCAATCC 2668  
 Oy 2609 GCGAGGTGCACTGACATGAGAGCTGTGTGTGTGAGAACCTGATTCGATTCGATC 2659  
 Db 2669 GCGAGGTGAGACCGCTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 2728  
 Oy 2669 GTCCGTAGACAGATGAGACCGGACGTAAGGAGCGCTCTTGTGACAGATATGAGATG 2719  
 Db 2729 TTGAGAGATATGGAATGTTTTTTTCTTTTCTTTTGTGGAGGAGATATGGAATG 2788  
 Oy 2720 TTGTCACTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2775  
 Db 2789 TT---AACTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2845  
 Oy 2776 TTAATCT---GTTAAGTGGAGCAAGGCGGAGGAGTACATG 2821  
 Db 2846 TTAATCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2895  
  
 RESULT 8  
 ABR8113  
 ID ABR8113 standard; cDNA; 2950 BP.  
 XX  
 AC ABR8113;  
 DT 07-OCT-2002 (first entry)  
 XX  
 DE cDNA encoding barley line MK6827 starch synthase II (SSII).  
 XX  
 KM Barley; starch synthase II; SSII; high amylose; reduced amylopectin;  
 KM food production; swelling volume; gelatinisation temperature;  
 KM reduced swelling; reduced viscosity; low crystallinity; instant noodle;  
 KM V form starch crystallinity; dietary fibre; instant soup; gene; ss;  
 KM line MK6827.  
 XX  
 OS Hordeum vulgare.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 107..2548  
 FT /\*tag= a  
 FT /product= "SSII"  
 FT /note= "Starch synthase II"  
 FT /transl\_except= (pos:233..235, aa:Xaa)  
 FT /note= "Encodes in frame stop codon"  
 XX  
 PN MO200237955-A1.  
 XX  
 PD 16-MAY-2002.  
 XX  
 PF 09-NOV-2001; 2001MO-AU001452.  
 XX  
 PR 09-NOV-2000; 2000AU-00001370.  
 PR 09-NOV-2000; 2000AU-00001371.  
 PR 09-NOV-2000; 2000AU-00001372.  
 PR 09-NOV-2000; 2000AU-00001373.  
 XX  
 PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 XX  
 PI Morell MK, Topping D, Batey IL;  
 DR MPI; 2002-557434/59.  
 DR P-PSDB; AAU99847.  
 XX  
 PT New barley plant for producing starch with improved characteristics, has  
 PT reduced level of SSII activity and is capable of bearing grain.  
 XX  
 PS Example 1; Fig 11; 107pp; English.  
 CC The invention describes a barley plant (I) with a reduced level of starch





Qy	183	CAACCTCTCCCTGCGGAGAGCTGAGACTCCGAGCAAGCGGCAATGACAGAGAGCCCTTCACACG	1896
Db	1897	CAACTTCTCCCTGAGAGAGCTGAGACTCCGAGCAAGCGGCAATGAGAGAGCCCTTCACACG	1956
Qy	1897	CGAGCTGGGACCTTCAGAGTCTCCGCGGCAAGCTGCTGGCTTCCTCATGAGCCGCTTGGAG	1956
Db	1957	CGAGCTGGGAGCTTCAGAGTCTCCGCGGCAAGCTGCTGGCTTCCTCATGAGCCGCTTGGAG	2016
Qy	1957	CGAGCGAAGAGGCGGAGAGTATCATGCGGAGCGCCATCCCTGGATGTTAGGACAGAGAGT	2016
Db	2017	CGAGCGAAGAGGCGGAGTATCATGCGGAGCGCCATCCCTGGATGTTAGGACAGAGAGT	2076
Qy	2017	GCAGCTGGTTCATGCTTGGGACACCGGCGGCAAGACTTGGAGAGAGATGCTTCGCGCATTTTGA	2076
Db	2077	GCAGCTGGTTCATGCTTGGGACACCGGCGGCGCAAGACTTGGAGAGAGATGCTTCGCGCATTTTGA	2136
Qy	2077	GCGGGAGACACAGACAGAGTTCGCGGAGTGGGTGGGATTTCCGTCGCGCTGGCGCACCG	2136
Db	2137	GCGGGAGACACAGACAGAGTTCGCGGAGTGGGTGGGATTTCCGTCGCGCTGGCGCACCG	2196
Qy	2137	GATTCAGAGGCGGCGGCGGCAAGCGGCTTCATATGCTCTCCCGGTTCGAGCCGCTGGCGGTGAA	2136
Db	2197	GATTCAGAGGCGGCGGCGGCGGCAAGCGGCTTCATATGCTCTCCCGGTTCGAGCCGCTGGCGGTGAA	2256
Qy	2197	CGAGCTTTACGCAATGAGCTCAAGGACAGTCCCGGCTGATGACAGCGCGGTGGCGGAGTAG	2256
Db	2257	CGAGCTTTACGCGATGAGCTCAAGGACAGTCCCGGCTGATGACAGCGCGGTGGCGGAGTAG	2316
Qy	2257	GGACACCGGTGGCGGCGGCTTCGACCCCTTCACACATTCGCGGCTTCGGGTGAGAGCTTTGACCG	2316
Db	2317	GGATACCGGTGGCGGCGGCTTCGACCCCTTCACACATTCGCGGCTTCGGGTGAGAGCTTTGACCG	2376
Qy	2317	CGCGGAGCGCACAAAGCTGATCGAGGCGCTTCGAGCACTGCTCCGACCTCACCGAGCTA	2376
Db	2377	CGCGGAGCGCACAAAGCTGATCGAGGCGCTTCGAGCACTGCTCCGACCTCACCGAGCTA	2436
Qy	2377	CAGAGAGACTGAGAGAGGCGCTTCAGAGAGCGGAGATGTCGAGAGAGATTTCAGTGGAGACA	2436
Db	2437	CAGAGAGACTGAGAGAGGCGCTTCAGAGAGCGGAGATGTCGAGAGAGATTTCAGTGGAGACA	2496
Qy	2437	TGCGGCGAAAGCTCTACGAGAGAGTCTGTCTCAGGCGCAACTACAGTGGTGAAC----	2496
Db	2497	TGCGGCGAAAGCTCTACGAGAGAGTCTGTCTCAGGCGCAACTACAGTGGTGAAC----	2556
Qy	2497	TGCTACCGGCTTCAGACCCCGGATGCGTGGCAATGAGAGGCTGGAACCTGCGCATTTGCGC	2556
Db	2553	TGCTACCGGCTTCAGACCCCGGATGCGTGGCAATGAGAGGCTGGAACCTGCGCATTTGCGC	2608
Qy	2557	CC-----GCAGGAACGTGCGCATCTTCGATGGAAGCGCGCGCATCC	2559
Db	2609	ACTTGCAGATTGCGGCAATGAGGAACGTGCGCGCTTCCTTGTGATGGGAACGCGCGCATCC	2668
Qy	2609	GGAGAGTGAAG-----TGAATGAGAGAGGTGTGGTGTGAGAGCGTCAATTCGAGTCTGA	2655
Db	2669	GGAGAGTGTGAGAGCTGATTCGCGATTCGTCCGTCGAGAGTGAAGTGAACGCTCTTGG	2728
Qy	2669	TCTGTGCTCGTAGAGAGTGAAGCGGAGCGTAGGAGAGCGTCTTGTGTGAGGATATAGG	2715
Db	2729	TTCAGAGTATATAGGAGATGTTTTTTTTTCTTTTCTTTTCTTTTGTGAGGAGGATATAGG	2788
Qy	2716	AAGTGTGATCACTGGATATGTGATTTGCTATGTTATGATAGCGTTATTA-----ATGTG	2771
Db	2789	AATGTT-----AAGTGTGATTTGATATGTGATTTGCTATGTTATGATAGCGTTATTA-----	2845
Qy	2772	TTCATTAATCTT-----GTTAAGTCGAGGCAAGAGGCGAAAGCTTAAGTCAATG	2821
Db	2846	TTCATTAATCTTGTAGTAAAGTCAAGTCCGAGGCGAAGAGCGAAAGCTTAAGTCAATG	2899
RESULT 9			
ABK88114			
ID ABK88114 standard; cDNA; 2951 BP.			
XX			

AC	AKR8814;
AD	
AE	
AF	
AG	
AH	
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AJ	
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Db 2317 GGNATCGGCGCCGCTTCGACCCCTTCAACCACTCGGGCTCGGGTGAAGCTTCGACCG 2376  
 Qy 2317 CGCCGAGCCGCAACAAGTGTATCGAGCGCTCGGCACTGCTCTCGGACCTTACCGGAGACTA 2376  
 Db 2377 CGCCGAGCCGCAACAAGTGTATCGAGCGCTCGGCACTGCTCTCGGACCTTACCGGAGACTA 2436  
 Qy 2377 CAAGGAGAGCTGAGAGGCGCTCTCGAGAGCGCGCATGCGCAGAGCTTCACTGCGAGCA 2436  
 Db 2437 CAAAGAGAGCTGAGAGGCGCTCTCGAGAGCGCGCATGCGCAGAGCTTCACTGCGAGCA 2496  
 Qy 2437 TGCCGCCAAGCTCTTACGAGAGCGTCTCTTCAAGGCCAAGTACCAAGTGTGAAGCGTACG 2496  
 Db 2497 TGCCGCCAAGCTCTTACGAGAGCGTCTCTTCAAGGCCAAGTACCAAGTGTGAAGCGTACG 2552  
 Qy 2497 TGCTAGCCGCTCGAGCCCGCATGCGATGATGAGAGGAGTGAAGCTGCGCATTTGCGC 2556  
 Db 2553 TGCTAGCCGCTCGAGCCCGCATGCGATGATGAGAGGAGTGAAGCTGCGCATTTGCGC 2608  
 Qy 2557 CC-----GCAAGAACGTGCCATCTCTTCTGATGGAGCGCGCGCATCC 2599  
 Db 2609 ACTTCAGATTGTGGCGCATGCGAGAACGTGCCGTCTTCTTGTATGGAGACCGCGCATCC 2668  
 Qy 2609 GCGAGTGCAGTGAACATGAGAGAGGTGTGTGTGAGACGCTGATCCGATCTGATCTG 2659  
 Db 2669 GCGAGTGCAGTGAACGCTGATCCGATCTGTCCGTGCGAGATGAGAGTGAAGCGCTCTG 2728  
 Qy 2669 GTCCGTACAGAGTGAAGCGGACGTAGGGAAGCGCTCTGTGTC---AGTATATGG 2714  
 Db 2729 TTGCAAGTATATGGAAATGTTTTTTTTTTTCTTTTTCGAGAGGAGTATATGG 2788  
 Qy 2715 GAATGTGTCACTGTGATTTGATTTGCTATGTTATGATGATTTTACA---ANGTT 2770  
 Db 2789 GAATGTT---AACTGTGATTTATATGTTGATGCTGTGATTTATTTACATCGGTTGT 2845  
 Qy 2771 GTTACTTATTTCTT---GTTAAGTGCAGGCAAGAGGCGAAAGCTAGCTCAATG 2821  
 Db 2846 GTTGTATTTCTTGTGATGATAGTGCAGAGCGCAAGAGCTAGCTCAATG 2900  
 RESULT 10  
 AAC86412  
 ID AAC86412 standard; cDNA; 2107 BP.  
 AC AAC86412;  
 XX 01-MAR-2001 (first entry)  
 DT  
 XX Wheat starch synthase II coding sequence SEQ ID NO: 5.  
 DE  
 XX Wheat; starch synthase; SSII; SSII; starch content; starch synthesis;  
 KM food product; adhesive; ss.  
 XX  
 OS Triticum aestivum.  
 XX  
 PN MO200066745-A1.  
 XX  
 PD 09-NOV-2000.  
 PF 28-APR-2000; 2000MO-AU000385.  
 PR 29-APR-1999; 99AU-00000052.  
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
 PA (GOOD-) GOODMAN FIELDER LTD.  
 PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.  
 XX  
 PI Morell M, Li Z, Rahman S, Appels R;  
 XX  
 DR WPI, 2000-647602/62.  
 DR P-PSDB; AAB37568.  
 XX  
 PT Nucleic acid molecules encoding wheat starch synthase (WST-I and WST-II,

PT useful in modifying plant starch content and/or composition.  
 XX  
 PS Claim 1; Page 161-163; 211pp; English.  
 XX  
 CC The present invention relates to novel protein and coding sequences from  
 CC wheat. The proteins are wheat starch synthases, designated SSII and  
 CC SSIII. These can be used in the modification of plant starch content or  
 CC composition, and to screen plants to identify mutations which affect  
 CC starch content and composition. The starch can then be used in food  
 CC products, such as flour, and in films, coatings, adhesives, building  
 CC materials and packaging materials  
 XX  
 SQ Sequence 2107 BP; 452 A; 566 C; 664 G; 425 T; 0 U; 0 Other;  
 Query Match 64.3%; Score 1828.4; DB 3; Length 2107;  
 Best Local Similarity 93.3%; Pred. No. 0;  
 Matches 2005; Conservative 0; Mismatches 91; Indels 52; Gaps 7;  
 Qy 695 CCAGCCGAGAGACCCCGCGCTGTCGCGCTCAAAATTTGATGCTCGGCTTGTGCTCC 754  
 Db 1 CAGCTGAGAGAACCCCGCGCTGTCGCGCTCAAAATTTGATGCTCGGCTTGTGCTCC 60  
 Qy 755 AGGCTGACATTTGACAGCGATGTTGAACCTGAAGAGAGGTCGCTATCGTCAA 814  
 Db 61 GGGTCTGACACTGTGACGACGCTGGAACAAAGTGAAGAGGTCGCTGTTGCA 120  
 Qy 815 GAAGCTCAAAACCCAAAGGCTCTTTCGCGCTGACGCCCGCTGTAACAAGACCTT 874  
 Db 121 GAAGCTCAAAACCCAAAGGCTCTTTCGCGCTGACGCCCGCTGTAACAAGACCTT 180  
 Qy 875 TGGGACTTCAAGAAATACATTTGCTTGAAGACCCCGTGAAGCCAGATATGCTCG 934  
 Db 181 TGGGATTTCAAGAAATACATTTGCTTGAAGACCCCGTGAAGCCAGATATGCTCG 240  
 Qy 935 GCTGTGACAGATGATGCGGCGCTCCTTGAACATCAACAGACATGATCCGACCTTG 994  
 Db 241 GCTGTGACAGATGATGCGGCGCTCCTTGAACATCAACAGACATGATCCGACCTTG 300  
 Qy 995 GCAAGGAGAGACGTATGAACGTGTCGTGTCGTGCTGAATGTTCTCCTGTGCAAA 1054  
 Db 301 GCAAGGAGAGATGATGAACGTGTCGTGTCGTGCTGAATGTTCTCCTGTGCAAA 360  
 Qy 1055 ACAAGTGTGTTGAGATATGTCGCGGTGCTTGGCCCAAGCTTGGCGAAGAGACAT 1114  
 Db 361 ACAAGTGTGTTGAGATATGTCGCGGTGCTTGGCCCAAGCTTGGCGAAGAGACAT 420  
 Qy 1115 CGTGTATGTTGTGTACCAAGTATGAGGACTATGAGAAAGCTTACGATGTGAGTGC 1174  
 Db 421 CGTGTATGTTGTGTACCAAGTATGAGGACTATGAGAAAGCTTACGATGTGAGTGC 480  
 Qy 1175 CGAAATATCTAACAGCTGTGACAGATATGAGAGTGAATTTTCCATGCTTATTC 1234  
 Db 481 CGAAATATCTAACAGCTGTGACAGATATGAGAGTGAATTTTCCATGCTTATTC 540  
 Qy 1235 GATGAGTGTATTTGTGTCATTTGACGCTCTCTCTCGACACCGCGCAAGACATT 1294  
 Db 541 GATGAGTGTATTTGTGTCATTTGACGCTCTCTCTCGACACCGCGCAAGACATT 600  
 Qy 1295 TATGAGGCGACAGACAGAAATTAAGAGCGATATTTGTTTGGCAAGGCGCGTTC 1354  
 Db 601 TATGAGGCGACAGACAGAAATTAAGAGCGATATTTGTTTGGCAAGGCGCGTTC 660  
 Qy 1355 GAGGTTCTTGGCAGCTTCATGCGGCGGTGTCTTATGAGGAGTGAATCTGTGTTT 1414  
 Db 661 GAGGTTCTTGGCAGCTTCATGCGGCGGTGTCTTATGAGGAGTGAATCTGTGTTT 720  
 Qy 1415 ATTGCAATGATTTGGCAGACGCGCATCTCTGCTGTCTATTTGAAGATTTTACAGGAC 1474  
 Db 721 ATTGCAATGATTTGGCAGACGCGCATCTCTGCTGTCTATTTGAAGATTTTACAGGAC 780  
 Qy 1475 CATGTTTGAATGAGTACATCGGTCATATGATGATGATATCAATAACATCGGACCAAGG 1534  
 Db 781 CATGTTTGAATGAGTACATCGGTCATATGATGATGATATCAATAACATCGGACCAAGG 840

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QY 1535 CGTGGCCCAATGATGTAATCCCGTTGACCGAGTTGGCTGAGCACTACCTGGAAACACTTTC 1594
DB 841 CGTGGCCCAATGATGTAATCCCGTTGACCGAGTTGGCTGAGCACTACCTGGAAACACTTTC 900
QY 1595 AGACTGTACGACCCCGTGGGTGTGAGACCGCAACTACTTTCGCCCGCTGAAAGATG 1654
DB 901 AGACTGTACGACCCCGTGGGTGTGAGAACCGCAACTACTTTCGCCCGCTGAAAGATG 960
QY 1655 GCGGACCAAGTTGTCGTGTGTGAGCCCGGGGTAACCTGGAGGCTCAAGAGGTGAGAGG 1714
DB 961 GCGGACCAAGTTGTCGTGTGTGAGCCCGGGGTAACCTGGAGGCTGAAAGAGGTGAGAGG 1020
QY 1715 GGGTGGGGGCTTTCAGCATCATACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1774
DB 1021 GGGTGGGGGCTTTCAGCATCATACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1775 GGCATCGACCAATGAGAGTGGAAACCGGAGGTGGACGTCACCTCAAGTGGAGAGGCTAC 1834
DB 1081 GGCATCGACCAATGAGAGTGGAAACCGGAGGTGGACGTCACCTCAAGTGGAGAGGCTAC 1140
QY 1835 ACCAATTCTCCCTGGAGAGCGCTGAGCTCCCGCAAGCGGAGTCAAGAGAGGCTTGAG 1894
DB 1141 ACCAATTCTCCCTGGAGAGCGCTGAGCTCCCGCAAGCGGAGTCAAGAGAGGCTTGAG 1200
QY 1895 CGCGAGCTGGGCTTGCAGAGTCCCGGCGGAGCTGGCTGGCTTCACTCGGCGGCTG 1954
DB 1201 CGCGAGCTGGGCTTGCAGAGTCCCGGCGGAGCTGGCTGGCTTCACTCGGCGGCTG 1260
QY 1955 GACGCGGAGAGAGGCGTGGAGATCATCGGAGAGCGCATGCTCGATCGTGGAGCAGAGAC 2014
DB 1261 GACGCGGAGAGAGGCGTGGAGATCATCGGAGAGCGCATGCTCGATCGTGGAGCAGAGAC 1320
QY 2015 GTGCACTGTGTATCTGTGGGACCGGCGGCGGACCGACTGCTGAGAGAGATCTGCGGCACTTC 2074
DB 1321 GTGCACTGTGTATCTGTGGGACCGGCGGCGGACCGACTGCTGAGAGAGATCTGCGGCACTTC 1380
QY 2075 GAGCGGAGAGACCAAGAGAGTGGCGGAGTGGAGTGGAGTCTCGGAGCGGCTGAGCGAC 2134
DB 1381 GAGCGGAGAGACCAAGAGAGTGGCGGAGTGGAGTGGAGTCTCGGAGCGGCTGAGCGAC 1440
QY 2135 CGGATTCACGCGCGGCGGCGGCGGCTCTCATGCTCTCGGCTCTCGGCTCTCGGCTCTG 2194
DB 1441 CGGATTCACGCGCGGCGGCGGCGGCTCTCATGCTCTCGGCTCTCGGCTCTCGGCTCTG 1500
QY 2195 AACGAGCTTACGCACTGAGCTTACGAGACCGTCCCGTGTGCAAGCGGCTGAGCGGAGT 2254
DB 1501 AACGAGCTTACGCACTGAGCTTACGAGACCGTCCCGTGTGCAAGCGGCTGAGCGGAGT 1560
QY 2255 AGGAGACACCGTGGCGGCTTTCAGACCCCTTCAACACTCCCGGCTGAGGAGCGTTCAGC 2314
DB 1561 AGGAGACACCGTGGCGGCTTTCAGACCCCTTCAACACTCCCGGCTGAGGAGCGTTCAGC 1620
QY 2315 CGGCGGAGAGGCGGAGAGTGTGAGGCGCTCGGAGCACTGCTCGGCACTTACCGGAGC 2374
DB 1621 CGGCGGAGAGGCGGAGAGTGTGAGGCGCTCGGAGCACTGCTCGGCACTTACCGGAGC 1680
QY 2375 TACAGAGAGAGTGTGAGGAGGCGCTTTCAGAGACCGGAGTGTGAGAGAGCTTCACTG 2434
DB 1681 TACAGAGAGAGTGTGAGGAGGCGCTTTCAGAGACCGGAGTGTGAGAGAGCTTCACTG 1740
QY 2435 GATGCGGCGCAAGCTTACAGAGAGAGTCTCTCAAGGCGCAAGTGTGAGAGAGCTA 2494
DB 1741 GATGCGGCGCAAGCTTACAGAGAGAGTCTCTCAAGGCGCAAGTGTGAGAGAGCTA 1800
QY 2495 GCTGTAGAGCGCTTCAGGCGCGGATGCTGATGATGAGAGAGTGAATCTGCGATTC 2554
DB 1801 GCTGTAGAGCGCTTCAGGCGCGGATGCTGATGATGAGAGAGTGAATCTT--GCAATTC 1854
QY 2555 GCGCGGAGAGAGTGTGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2614
DB 1855 GCAAGGAGAGAGTGTGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1903

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QY 2615 ATGAGAGTGTGTGTGTGTGAGAGAGCTGATTCGATCTCGATCTGTCGAGAGAGTA 2674
DB 1904 AT--GAGGTGTGTGTGTGTGAGAGAGCTGATTC-----CAATCGGCGCGGAGAGAGTA 1955
QY 2675 GAGCGGAGCTAGGAGAGAGCGCTCTTGTGACGATATAGGAGATGTGTCAACTTGGAT 2734
DB 1956 GAGCGG-----AGGATATGGGATCTT--AACTTGTAT 1988
QY 2735 TGTACTTGTATGTTGTATGTCGTTATTAATGATGTTACTTATCTTGTATGAGGA 2794
DB 1989 TGTATTTGTATGTTGTGTGTCATTTATTAATGATGTTACTTATCTTGTATGAGGA 2048
QY 2795 GGCAGAGGCGGAGAGCTAGCTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2842
DB 2049 GGCAGAGGCGGAGAGCTAGCTCACTGATGTGTATGAGAGAGAGAGAGAGAGAG 2096

RESULT 11
AAC8434
ID AAC8434 strand; cDNA; 2107 BP.
XX
XX AAC8434;
AC
XX 01-MAR-2001 (first entry)
DT
XX
DE Wheat starch synthase clone WSIIIB cDNA.
XX
XX Wheat; starch synthase; SSII; SSIII; starch content; starch synthesis;
KM food product; adhesive; ss.
XX
XX Triticum aestivum.
OS
XX MO200066745-A1.
PN
XX 09-NOV-2000.
PD
XX
XX 28-APR-2000; 2000WO-AD000385.
PF
XX
XX 29-APR-1999; 99AU-00000052.
PR
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
PA (GOOD-) GOODMAN FIELDER LTD.
PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
PI
PI Morell M, Li Z, Rahman S, Appels R;
XX
XX WPI: 2000-647602/62.
DR
XX
XX Nucleic acid molecules encoding wheat starch synthase (WST)-I and WST-II,
PT useful in modifying plant starch content and/or composition.
PS
PS Disclosure; Fig 2; 21pp; English.
PS
XX
XX The present invention relates to novel protein and coding sequences from
CC wheat. The proteins are wheat starch synthases, designated SSII and
CC SSIII. These can be used in the modification of plant starch content or
CC composition, and to screen plants to identify mutations which affect
CC starch content and composition. The starch can then be used in food
CC products, such as flour, and in films, coatings, adhesives, building
CC materials and packaging materials
XX
XX Sequence 2107 BP; 452 A; 566 C; 664 G; 425 T; 0 U; 0 Other:
SQ
Query Match 64.3%; Score 1828.4; DB 3; Length 2107;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 2005; Conservative 0; Mismatches 91; Indels 52; Gaps 7;
QY 695 CCAGCCGAGAGAGCGCGCGCTGTGTGCGGCTCAAAATTTGCTGTGCTGCTGCTGCC 754
DB 1 CCAGCTGAGAGAGAGCGCGCGCTGTGTGCGGCTCAAAATTTGAGATCTGCGGCTGCTGCC 60
QY 755 AGGCTGAGCATTTGACAGAGTGTGAACCTGAACCTGAAGAGAGTGGCTCATGTGAA 814

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Db 61 GGGCTGACACTGTCAGAGCAGTGGAAACAAGAACTGAAGAGGGTGGGCTGTGTGCAA 120  
Qy 815 GAACTCCAAACCCAAAGGCTCTTTCGGCGCTGAGCGCCGGGTGTAACAAGAACTT 874  
Db 121 GAACTCCAAAGCCAAAGGCTCTTTCGGCGCTGAGCGCCGGGTGTAACAAGAACTT 180  
Qy 875 TGGGACTTCAAGAAATATACATTGGCTTTCAGAGAGCCCGTGAAGGCCCAAGATGATGGCTG 934  
Db 181 TGGGATTTCAAGAAATATACATTGGCTTTCAGAGAGCCCGTGAAGGCCCAAGATGATGGCTG 240  
Qy 935 GCTGTTCGATGATAGCCGGGCTCTTTCGATGATGACCAAGAACCATGATTCGGGACTTGG 994  
Db 241 GCTGTTCGATGATAGCCGGGCTCTTTCGATGATGACCAAGAACCATGATTCGGGACTTGG 300  
Qy 995 GCAGGAGAGAACTGATGAACTGGTCTGCTGCTGCTGATGATGCTTCTCTGATGCAA 1054  
Db 301 GCAGGAGAGAACTGATGAACTGGTCTGCTGCTGCTGATGATGCTTCTCTGATGCAA 360  
Qy 1055 AACAGTGTCTTGGAGATGTTCCCGTGTCTTTCGCAAGGCTTTGGCAAGAGAGCAT 1114  
Db 361 AACAGTGTCTTGGAGATGTTCCCGTGTCTTTCGCAAGGCTTTGGCAAGAGAGCAT 420  
Qy 1115 CGGTGTAATGTTGTGTGTAACAAGTATGAGGAGCTATGAGAAAGCTTACGATGTGAGATC 1174  
Db 421 CGGTGTAATGTTGTGTGTAACAAGTATGAGGAGCTATGAGAAAGCTTACGATGTGAGATC 480  
Qy 1175 CGAAATATCTAACAGGCTGCTGAGCAAGATATGAAATGAAATTTATTTCCATGCTTATATC 1234  
Db 481 CGAAATATCTAACAGGCTGCTGAGCAAGATATGAAATGAAATTTATTTCCATGCTTATATC 540  
Qy 1235 GATGAGTGTATTTGTGTGTAACAAGTATGAGGAGCTTCTTCCGACACCGCAGAGAGACAT 1294  
Db 541 GATGAGTGTATTTGTGTGTAACAAGTATGAGGAGCTTCTTCCGACACCGCAGAGAGACAT 600  
Qy 1295 TATGAGGAGCAGCAGCAAGAAATTATGAAGCGCATGATTTGTTCTGCAAGGCGCTGTC 1354  
Db 601 TATGAGGAGCAGCAGCAAGAAATTATGAAGCGCATGATTTGTTCTGCAAGGCGCTGTC 660  
Qy 1355 GAGTTCCTTGGCAGCTTCCATGCGCGGCTGCTCCCTTATGAGGAGTGAATGAGTGTGTT 1414  
Db 661 GAGTTCCTTGGCAGCTTCCATGCGCGGCTGCTCCCTTATGAGGAGTGAATGAGTGTGTT 720  
Qy 1415 ATTGCAATGATTTGCAACGCGGACCTCTGCTGTCTATCTGAAAGCATATTTACAGGAGC 1474  
Db 721 ATTGCAATGATTTGCAACGCGGACCTCTGCTGTCTATCTGAAAGCATATTTACAGGAGC 780  
Qy 1475 CATGTTTGAATGATGATCACTGCTGCTATTAATGATGATGATGATGATGATGATGATG 1534  
Db 781 CATGTTTGAATGATGATCACTGCTGCTATTAATGATGATGATGATGATGATGATGATG 840  
Qy 1535 CGTGGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1594  
Db 841 CGTGGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900  
Qy 1595 AGACTGTACGACCCCGTGGTGTGAGCAAGCCACTTACTTGGCCGCGCTGAAAGATG 1654  
Db 901 AGACTGTACGACCCCGTGGTGTGAGCAAGCCACTTACTTGGCCGCGCTGAAAGATG 960  
Qy 1655 GCGGACCAAGTGTGCTGCTGAGAGCCCGGCTGCTGAGGAGTCAAGAGCGTGAAGGCG 1714  
Db 961 GCGGACCAAGTGTGCTGCTGAGAGCCCGGCTGCTGAGGAGTCAAGAGCGTGAAGGCG 1020  
Qy 1715 GGTGTGGGGGCTTCAACGATCATACGAGAGAGCATGAGAGCCCGGCTGATGATG 1774  
Db 1021 GGTGTGGGGGCTTCAACGATCATACGAGAGAGCATGAGAGCCCGGCTGATGATG 1080  
Qy 1775 GGTGTGGAGCAACATGAGTGGAGAACCCGAGTGGAGCTTCAAGTCCGAGGCTGATG 1834  
Db 1081 GGTGTGGAGCAACATGAGTGGAGAACCCGAGTGGAGCTTCAAGTCCGAGGCTGATG 1140  
Qy 1835 ACCAATCTTCTCTGAGGAGCGTGAATCCGCGCAAGGAGGAGTGAAGAGGCTTGAAG 1894  
Db 1141 ACCAATCTTCTCTGAGGAGCGTGAATCCGCGCAAGGAGGAGTGAAGAGGCTTGAAG 1200

Qy 1895 CCGAGACTGGGCTTGAAGTCCGCGCCGACGATGCGCTGCTGAGTCTTATGAGGCGCTG 1954  
Db 1201 CCGAGACTGGGCTTGAAGTCCGCGCCGACGATGCGCTGCTGAGTCTTATGAGGCGCTG 1260  
Qy 1955 GACGGGCAAGAGGGGTGAGATCAATCGCGAGCGCATGAGCTTGAATGATGAGGAGGAG 2014  
Db 1261 GACGGGCAAGAGGGGTGAGATCAATCGCGAGCGCATGAGCTTGAATGATGAGGAGGAG 1320  
Qy 2015 GTGCACTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2074  
Db 1321 GTGCACTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380  
Qy 2075 GAGCGGAGACCAACGACAAAGTGGCGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 2134  
Db 1381 GAGCGGAGACCAACGACAAAGTGGCGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1440  
Qy 2135 CGGATCAAGGCGGCGCGGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2194  
Db 1441 CGGATCAAGGCGGCGCGGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500  
Qy 2195 AACCACTTTAAGCCATGAGCTTACGAGCAACGCTTCCGCTGCTGCTGCTGCTGCTGCTG 2254  
Db 1501 AACCACTTTAAGCCATGAGCTTACGAGCAACGCTTCCGCTGCTGCTGCTGCTGCTGCTG 1560  
Qy 2255 AGGAGCAAGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2314  
Db 1561 AGGAGCAAGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620  
Qy 2315 CCGCGGAGGCGCAACAGCTGATGAGGCGCTTGGGACATGCTTCCGCGACCTTACCGGAGC 2374  
Db 1621 CCGCGGAGGCGCAACAGCTGATGAGGCGCTTGGGACATGCTTCCGCGACCTTACCGGAGC 1680  
Qy 2375 TACAAGAGAGCTGAGAGGCGCTTCCAGAGCGGCGATGCTGAGAGACTTACGCTGAGAG 2434  
Db 1681 TACAAGAGAGCTGAGAGGCGCTTCCAGAGCGGCGATGCTGAGAGACTTACGCTGAGAG 1740  
Qy 2435 CATGCGCCAAAGCTTACAGAGAGCTTCTTCAAGGCGCAAGTACAGTGTGTAAGCTTA 2494  
Db 1741 CATGCGCCAAAGCTTACAGAGAGCTTCTTCAAGGCGCAAGTACAGTGTGTAAGCTTA 1800  
Qy 2495 GCTGCTAGCGGCTTCCAGGCGCGGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2554  
Db 1801 GCTGCTAGCGGCTTCCAGGCGCGGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1854  
Qy 2555 GCCCGCAAGAGCTGATCTTCTGATGAGAGCGCGGATGCGGAGTGAAGTGAAGTGAAGTGAAG 2614  
Db 1855 GCCCGCAAGAGCTGATCTTCTGATGAGAGCGCGGATGCGGAGTGAAGTGAAGTGAAGTGAAG 1903  
Qy 2615 ATGAGAGTGTGTGTGTGAGAGCGTGAATTCGATGCTGATGCTGATGCTGATGCTGATG 2674  
Db 1904 ATGAGAGTGTGTGTGTGAGAGCGTGAATTCGATGCTGATGCTGATGCTGATGCTGATG 1955  
Qy 2675 GAGCGAGCTAGAGGAGCGCTCTTGTGAGGATATGAGGATGTTGTCACTGCTGAT 2734  
Db 1956 GAGCGG-----AGGATATGGAATCTT---AATGCTGAT 1988  
Qy 2735 TGTAGTTGCTATGTTGATGAGCTTATTAACATGTTGTTATCTATCTTGTAGTGAAGTGA 2794  
Db 1989 TGTAGTTGCTATGTTGATGAGCTTATTAACATGTTGTTATCTTGTAGTGAAGTGAAGTGA 2048  
Qy 2795 GGCAGAGGCGGAAGCTAGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 2842  
Db 2049 GGCAGAGGCGGAAGCTAGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 2096

RESULT 12  
ACCT0869  
ID ACCT0869 standard; DNA; 2607 BP.  
XX  
XX ACCT0869;  
XX  
DT 20-NOV-2003 (first entry)

XX Rice starch synthase Iia coding sequence.  
 DE  
 XX Rice, starch synthase Iia; starch; crop; plant; gene; ds.  
 KM  
 XX Oryza sativa.  
 OS  
 XX Key Location/Qualifiers  
 FH 103..2535  
 FT CDS /\*tag=a  
 FT /product="Rice starch synthase Iia"  
 FT  
 XX MO2003023024-A1.  
 PN  
 XX  
 XX 20-MAR-2003.  
 PD  
 XX 10-SEP-2002; 2002MO-JP009221.  
 PF  
 XX 10-SEP-2001; 2001JP-00273166.  
 PR 10-SEP-2001; 2001JP-00277109.  
 PR 12-SEP-2001; 2001JP-00277120.  
 PR 20-SEP-2001; 2001JP-00287010.  
 XX  
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 PA  
 XX Nakamura Y, Fujita N, Satoh H;  
 PI WPI, 2003-371750/35.  
 DR P-PSDB; ABR56308.  
 DR  
 XX Genetically-modified starch synthases in enzyme systems for producing  
 PT novel starch with different properties e.g. paste-formation and taste,  
 PT useful in new breeds of crops including plants like rice.  
 XX  
 XX Example 5; Fig 19-20; 140pp; Japanese.  
 PS  
 XX The present sequence is the coding sequence for a rice starch synthase  
 CC Iia. The starch synthase Iia gene and its protein are useful for the  
 CC synthesis of novel starch with different properties, which are useful in  
 CC new breeds of crops including plants like rice  
 XX  
 XX Sequence 2607 BP; 482 A; 770 C; 891 G; 464 T; 0 U; 0 Other;  
 SQ  
 Query Match 45.6%; Score 1297.2; DB 7; Length 2607;  
 Best Local Similarity 72.6%; Pred. No. 1.5e-222;  
 Matches 1776; Conservative 0; Mismatches 640; Indels 30; Gaps 7;

Db 457 CCGCCCTCGGCGGTACGGCTCCGGGGTGAACGGGGGAGAGTGGCGGGGCGGCCG 516  
 Qy 479 GGTGAGAA CAAATCTTACCGGCGGGGGCGCCGACCAAAGACACGGGGCTGCCGACCC 538  
 Db 517 CCGGGCGGGGCGCCGACACAGAGAGCCCTCAAGATGAAGAGAGCGCTTCTAGCGGC 576  
 Qy 539 GCAAGGGGCGCCCATCGCTGACCCAGAACAGAGTACCAATGAAACGCTGAAAACAAAGCT 598  
 Db 577 CCGGACGACGACACACTGCTCTACAGAACGAGATCGGCTGTTACGGGGCGCGACAGGCT 636  
 Qy 599 AACGTGCTCGCGCGCGGACGACATAGCCCAAGTGTGGCTCCGAGATTCCGACGTACC 658  
 Db 637 GCCGCGGACACCGCCCGGTGACATAAGAGCTCCAGGCGCGGACTCCCGGTGATC 696  
 Qy 659 ATTTCATCAATGACAAAGGCG--GCCGAGTCCGTGTCCAGCGGAGAACCGCGCG 715  
 Db 697 CTTCATCTGTAGACAAAGCCGACGCGAGATTCTCATCCAGACGCGACGGCGCG 756  
 Qy 716 TCGTCGGGCTCAAAATTTGCTGTCTGGCTTCTGCTCCAGGCTGGAATTGACAGCAT 775  
 Db 757 CCGCCACCGCCGCTTCAAATCCAGAGTGTCTCGCTCTCCGACCTTGACA--AT 813  
 Qy 776 GTTGAACCTGAAGTGAAGAGGGTGGGTCATGTCGAAGAGCTCCAAACCAAGGCT 835  
 Db 814 TCGGAATTTGACAGAGATAGAGCCGAAAGTTGTTGAGAGTGTCCGAGCAAGGCG 873  
 Qy 836 CTTCGCGCGCTGACGCCCCCGCTGTACAGAGACCTTTGGAGCTTCAAGAAATTAATT 895  
 Db 874 ACTAGATCTTCCCTATTTCTCGGTAGAGAGAGACGTGGGATTTCAAGAAATTAATT 933  
 Qy 896 GGTTCGAGAGAGCCCTGAGAGCCAG-----GATGATGGGCTGGCTGTGCA 943  
 Db 934 GATCTAAGCAACCGGACCCCGGAGATGCGCATGACATGATGATGATGATGATGATGAT 993  
 Qy 944 GATGATGCGGCTCTTTGAACATCACAGAAACATGATTTCCGACCTTTGGACGGGAG 1003  
 Db 994 GATGCGTCAATTC---TGAGATGACAGAGATGAGATTCGGGCTTTGGCTGGGGAG 1050  
 Qy 1004 AACGTATGAACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1063  
 Db 1051 AATGTATGAACGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1110  
 Qy 1064 CTTCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123  
 Db 1111 CTTCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1170  
 Qy 1124 GTTGTGTACCAAGTATGAGGACTATGAGAAAGCTTACAGATGCTGCTGCTGCTGCTGCT 1183  
 Db 1171 GTTGTGTACCAAGTATGAGGACTATGAGAAAGCTTACAGATGCTGCTGCTGCTGCTGCT 1230  
 Qy 1184 TACAGGCTGCTGAGACAGATATGAGAGTGAATTTTCCAGTCTTATATGATGAGATT 1243  
 Db 1231 TACAGGCTGCTGAGACAGATATGAGAGTGAATTTTCCAGTCTTATATGATGAGATT 1290  
 Qy 1244 GATTGTGTTCAATGACGCT 1303  
 Db 1291 GATTGTGTTCAATGACGCT 1350  
 Qy 1304 AGCAGACAGGAATTAAGAGCGATGATTTTGTTCGACAGGCGCTGTGAGTTCCT 1363  
 Db 1351 AACGACAGGAATTAAGAGCGATGATTTTGTTCGACAGGCGCTGTGAGTTCCT 1410  
 Qy 1364 TGGACGTTCCAGTCCGCGGCTGCTTATGAGGATGAGAAATCTGGTGTATTGGAAT 1423  
 Db 1411 TGGACGTTCCAGTCCGCGGCTGCTTATGAGGATGAGAAATCTGGTGTATTGGAAT 1470  
 Qy 1424 GATTGGACAGGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1483  
 Db 1471 GATTGGACAGTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1530  
 Qy 1484 ATGAGTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1543  
 Db 1531 ATGAGTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1590



QY 1544 GTAGATGATATCCGGTTCACCGAGTGGCTTGAGCACTACCTGGAACAATTGAGACTGTAC 1603  
 DB 1591 GTAGATGATATCCCGTTCACCGAGTGGCTTGAGCACTACCTGGAACAATTGAGACTGTAC 1650  
 QY 1604 GACCCCGTGGTGGTGGAGCAGCCCACTTTCGCGCGCGCGCTGGAAGATGGCCGAGCAG 1663  
 DB 1651 GACCCCGTGGTGGTGGAGCAGCCCACTTTCGCGCGCGCGCTGGAAGATGGCCGAGCAG 1710  
 QY 1664 GTTGTGATGATGAGCCCGGAGTACTGTGGAGCTCAAGACGTGAGAGCGCGCTGGGCGG 1723  
 DB 1711 GTGTGATGATGAGCCCGGAGTACTGTGGAGCTCAAGACGTGAGAGCGCGCTGGGCGG 1770  
 QY 1724 CTTCACGATCATATACGGAGAGAGCACTGGAAGACCCCGGAGTGTCAAGCGCATGAC 1783  
 DB 1771 CTTCACGATCATATACGGAGAGAGCACTGGAAGAGAGCGCATGTGAACGGCATGAC 1830  
 QY 1784 AACATGAGTGAACCCCGAGTGAAGTCCACCTCAAGTGAAGCGCTACACCAACTTC 1843  
 DB 1831 TACCGGAGTGAACCCCGAGTGAAGTCCACCTCAAGTGAAGCGCTACACCAACTTC 1890  
 QY 1844 TCCTGGGAGCGCTGAGTCCGCGCAAGCGGCACTGCAAGAGAGCGCTGACCGGAGCTG 1903  
 DB 1891 ACCGTGGCGCTCGCTGAGTCCGCGCAAGCGGCAAGCGGCGCTGCAAGCGGAGCTG 1950  
 QY 1904 GGCGTGAAGTCCGCGGAGTGGCGGCTGCTGAGCTTCATGCGCGCGCTGAGCGGAG 1963  
 DB 1951 GGCGTGAAGTCCGCGGAGTGGCGGCTGCTGAGCTTCATGCGCGCGCTGAGCGGAG 2010  
 QY 1964 AAGGCGTGAAGTCAATCGCGGAGCGCATCCCTGAGTGTGAAGCGAGAGTGAAGTGTG 2023  
 DB 2011 AAGGCGTGAAGTCAATCGCGGAGCGCATCCCTGAGTGTGAAGCGAGAGTGAAGTGTG 2070  
 QY 2024 GTCAATGCTGGGAGACCGCGCGGAGCGCATGAGAGACATGCTGCGGAGCATGAGAGCGGAG 2083  
 DB 2071 GTGCTGCTGGGAGACCGCGCGGAGCGCATGAGAGAGTGTGAGAGCGGAGTGAAGCGGAG 2130  
 QY 2084 CACACGACAGAGTGGCGGAGTGGGAGTGTGCGGAGTGTGCGGAGCGAGCATGAGTGAAG 2143  
 DB 2131 CACACGACAGAGTGGCGGAGTGGGAGTGTGCGGAGTGTGCGGAGCGAGCATGAGTGAAG 2190  
 QY 2144 GGCGGCGGAGCGCGCTCTCATGCGCTCCCGGCTGAGAGCGTGGGAGTGAACCAAGTT 2203  
 DB 2191 GGCGGCGGAGCGCGCTCTCATGCGCTCCCGGCTGAGAGCGTGGGAGTGAACCAAGTT 2250  
 QY 2204 TACGCCATGCGCTTACCGGAGCGGTCCCGTGTGAGAGCGCGTGGGAGTGAAGCAAC 2263  
 DB 2251 TACGCCATGCGCTTACCGGAGCGGTCCCGTGTGAGAGCGCGTGGGAGTGAAGCAAC 2310  
 QY 2264 GTGCGCGGCTTGAACCCCTTCAACCACTCCGCGCTTGGGAGTGTGAGCGTGGCGGAG 2323  
 DB 2311 GTGCGCGGCTTGAACCCCTTCAACCACTCCGCGCTTGGGAGTGTGAGCGTGGCGGAG 2370  
 QY 2324 GGCGCAAGCTGATCGAGGCGCTCGGAGCACTGCGCTCCGACCTACCGGAGTGAAGAGAG 2383  
 DB 2371 GGCGCAAGCTGATCGAGGCGCTCGGAGCACTGCGCTCCGACCTACCGGAGTGAAGAGAG 2430  
 QY 2384 AGCTGAGAGGCGCTTCAAGAGCGCGGAGTGTGAGAGAGTGTGAGAGTGTGAGAGTGTG 2443  
 DB 2431 AGCTGAGAGGCGCTTCAAGAGCGCGGAGTGTGAGAGAGTGTGAGAGTGTGAGAGTGTG 2490  
 QY 2444 AAGCTTGAAGAGCGTCTCTCAAGGCGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2489  
 DB 2491 AAGCTTGAAGAGCGTCTCTCAAGGCGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2536

RESULT 13  
 ID ACCT0868  
 XX ACCT0868 standard; DNA: 2607 BP.  
 AC ACCT0868;  
 XX  
 DT 20-NOV-2003 (first entry)

XX DE Rice starch synthase Ila coding sequence.  
 XX KM Rice; starch synthase Ila; starch; crop; plant; gene; ds.  
 XX OS Oryza sativa.  
 XX FT Key Location/Qualifiers  
 FT CDS 103..2535  
 FT /tag= a  
 FT /product= "Rice starch synthase Ila"  
 PN WO2003023024-A1.  
 PD 20-MAR-2003.  
 XX PF 10-SEP-2002; 2002MO-UP009221.  
 XX PR 10-SEP-2001; 2001JP-00273166.  
 PR 12-SEP-2001; 2001JP-00277109.  
 PR 12-SEP-2001; 2001JP-00277120.  
 PR 20-SEP-2001; 2001JP-00287010.  
 XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 XX PI Nakamura Y, Fujita N, Satoh H;  
 XX DR WPI; 2003-371750/35.  
 DR P-PSDB; ABR56307.  
 XX PT Genetically-modified starch synthases in enzyme systems for producing  
 PT novel starch with different properties e.g. paste-formation and taste,  
 PT useful in new breeds of crops including plants like rice.  
 XX PS Example 5; Fig 19-20; 140pp; Japanese.  
 CC CC The present sequence is the coding sequence for a rice starch synthase  
 CC Ila. The starch synthase Ila gene and its protein are useful for the  
 CC synthesis of novel starch with different properties, which are useful in  
 CC new breeds of crops including plants like rice  
 CC XX  
 SQ Sequence 2607 BP; 484 A; 769 C; 888 G; 466 T; 0 U; 0 Other;  
 Query March 45.6%; Score 1294.8; DB 7; Length 2607;  
 Best Local Similarity 72.0%; Pred. No. 4.1e-222;  
 Matches 1762; Conservative 0; Mismatches 654; Indels 30; Gaps 5;  
 QY 68 GCCCGATCCCGGCGCGCGCATGCTGCGCGCGTGGCGCGTCCGCGCTCTCTCGCG 127  
 DB 97 GCGACATGCTGCTGCGCGCGTGGCGCGTCAACACAGTCTCTGCGCGTCTCTCT 156  
 QY 128 CTGCGCTCCCGCTCCCGGAGATACGAGCGCGGAGGTGAGCGCGCGCAACC 187  
 DB 157 TCGGCGTCAAGGAGGAGCCCAAGAGGAGGAGTGTGCGCGCGCGCGCGCGCG 216  
 QY 188 C-----ACGCGGCGCGCGCGCGCGCATGCGCGCGCGCGCGCGCGCGCGCG 238  
 DB 217 CTGCTTACAGACG 276  
 QY 239 GCTCGCAGAGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 298  
 DB 277 CGGCTTGGCGCGTGGAGTGGGAGCGTGGCGCGCGCGCGCGCGCGCGCGCGCG 336  
 QY 299 GACCGCGCGTCCGCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 358  
 DB 337 GCGGTGAGCG 396  
 QY 359 GAGCGAGGAGTCCGTCAGAGCGCTGATCGCGCGCGCGCGCGCGCGCGCGCGCG 418  
 DB 397 CAGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 456  
 QY 419 CCGCGCGCGCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 478



XX DE Corn starch synthase Ssb DNA fragment inserted in pSPB47.  
 XX XX Starch synthase; Ssb; starch fine structure; corn; transgenic plant;  
 XX XX amylose; amylopectin; amylose polymerization;  
 XX XX non-granule bound starch synthase; non-GBSSI; altered starch; food;  
 XX XX paper; plastic; adhesive; ss.  
 OS Zea mays.  
 XX XX WO200006755-A2.  
 XX XX 10-FEB-2000.  
 XX XX 26-JUL-1999; 99WO-US016296.  
 XX XX 28-JUL-1998; 98US-0094436P.  
 XX XX (DUPO) DU PONT DE NEMOURS & CO E I.  
 XX XX Biogile KE, Lightner JE;  
 XX XX WPI; 2000-195311/17.  
 XX XX Producing transgenic cereal crops with altered starch structure useful  
 XX XX for preparing foodstuff, paper, plastic or adhesives, comprises  
 XX XX transforming crops with chimeric sense or antisense gene construct  
 XX XX encoding starch synthase.  
 PS Claim 17; Page 56; 56pp; English.  
 XX XX The present sequence is a corn starch synthase Ssb 2248 bp insert in  
 XX XX clone pSPB47. Plasmid pSPB47 contains the entire Ssb cDNA in sense  
 XX XX orientation surrounded by the zein promoter and the zein 3' end. Purified  
 XX XX pSPB47 is introduced into corn callus culture cells. Transgenic corn  
 XX XX express altered starch structure. The starch fine structure derived from  
 XX XX a grain of the cereal crop can be altered in the transformed cereal crop  
 XX XX by changes in amylose to amylopectin ratio, amylopectin fine structure,  
 XX XX increased abundance of very short amylopectin chains and in the degree of  
 XX XX polymerisation of amylose. These modifications can be created by  
 XX XX controlling the expression of non-GBSSI (non-granule bound starch  
 XX XX synthase) in transgenic plants. Altered starches are useful in foods,  
 XX XX paper, plastics or adhesives  
 XX XX  
 XX XX Sequence 2248 BP; 434 A; 640 C; 722 G; 452 T; 0 U; 0 Other;  
 XX XX  
 XX XX Query Match 43.8%; Score 1246; DB 3; Length 2248;  
 XX XX Best Local Similarity 84.6%; Pred. No. 2.1e-213;  
 XX XX Matches 1399; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

QY 1200 AGGATATGAAAGTAATTTATTCATGCTTATATCATGAGTGAATTTGTGTCAATG 1259  
 DB 913 AGGACCTAAGATGAACTTTTCATGATATTTATGAGAGTGCACATTTGTGTCAATG 972  
 QY 1260 AGCTCCTCTCTCCGACACCGCGAGGAAGACATTTATGAGGAGCGACAGAGAAATTA 1319  
 DB 973 ATGCCCTCTTTTCCGACACCGCTCAAGATGACATATATGGGGAAGTATGAGGAATCA 1032  
 QY 1320 TGAAGCCATGATTTTGTCTGCAAGCGCGCTGTGAGATTCTTGGACGTTCCATGCG 1379  
 DB 1033 TGAAGGCAATGATTTTGTCTGCAAGGTTGCTGTGAGATTCTTGGACGTTCCATGCG 1092  
 QY 1380 GCGGTATGCCCTTATGAGGATGGAATCTGATGTTATGCAAAATGATGGACACGCGAC 1439  
 DB 1093 GTGGTGTGCTATACGAGATGGAATTTGTGTCTGATTCATTCGCAATGATGGACACTGAC 1152  
 QY 1440 TCCTGCTGTCTATCTGAAAGCATTTTACAGGACCATGTTGATGCAATCACTCGGT 1499  
 DB 1153 TCCTGCTGTCTTATCTGAAAGCATTTTACAGGACCATGTTGATGCAATCACTCGGT 1212  
 QY 1500 CCATATGATGATACATTAACATTCGACACAGGCGCGTGGCCAGATGATGATTCGGT 1559  
 DB 1213 CGGTCTGTGATACATTAACATTCGACACAGGCGCGTGGCCAGATGATGATTCGGT 1272  
 QY 1560 TCAACGATTTGCTTACGACATTCCTGGAACACTTTCAGACTGTACGACCCGTGGTGTG 1619  
 DB 1273 ACATGATCTTGTCTGACATCTTCAACATTTGAGCTGTACGATCCGTGGTGTGCG 1332  
 QY 1620 AGCACGCCAATCTTCCGCGCGCGCTGAAAGTGGCGGACCAAGTGTCTGTGTGAGCC 1679  
 DB 1333 AGCACGCCAATCTTCCGCGCGCGCTGAAAGTGGCGGACCAAGTGTGTGAGCC 1392  
 QY 1680 CCGGATACCTGTGAGAGCTCAAGACGCTGAGAGGCGGCTGGGGGCTTACGACATCATAC 1739  
 DB 1393 GCGGCTACCTGTGAGAGCTCAAGACGCTGAGAGGCGGCTGGGGGCTTACGACATCATAC 1452  
 QY 1740 GCGAGAACCATGGAAGACCCCGGACATCTGTCAACGCGATCGAACATGAGTGAAC 1799  
 DB 1453 GTTCTAACCATGGAAGACCATGAGATCTGTCAACGCGATCGAACATGAGTGAAC 1512  
 QY 1800 CCGAGGTGACCTGCACTCACTCAAGTGGACGAGACGCTTACCACTTCTCTTGGGACACGCTGG 1859  
 DB 1513 CCAAGGTGACCTGCACTCACTCAAGTGGACGAGACGCTTACCACTTCTCTTGGGACACGCTGG 1572  
 QY 1860 ACTCCGCAAGGCGGACGTCAGAGAGGCGCTTCAAGCGGACGAGTGGGCTTCAAGTCCGCG 1919  
 DB 1573 AGCTTGAAAGGCGGACGTCAGAGAGGCGCTTCAAGCGGACGAGTGGGCTTCAAGTCCGCG 1632  
 QY 1920 CCGACGTGCGCTGCTCGGCTTCAATCGGCGCGCTTCAAGCGGACGAGTGGGCTTCAAGTCCGCG 1979  
 DB 1633 ACACGCTGCGCTGCTCGGCTTCAATCGGCGCGCTTCAAGCGGACGAGTGGGCTTCAAGTCCGCG 1692  
 QY 1980 TCGCGAGCCCATGCGCTTCAATCGGCGCGCTTCAAGCGGACGAGTGGGCTTCAAGTCCGCG 2039  
 DB 1693 TCGCGAGCCCATGCGCTTCAATCGGCGCGCTTCAAGCGGACGAGTGGGCTTCAAGTCCGCG 1752  
 QY 2040 GCGCGCACCATGGAAGACATGCTGCGGACCTTGAACGCGGAGACCAACGAAAGTGC 2099  
 DB 1753 GCGCGCACCATGGAAGACATGCTGCGGACCTTGAACGCGGAGACCAACGAAAGTGC 1812  
 QY 2100 GCGGATGAGTGGAGTCTTCCGTCGCTGCGGACCGGANTCAAGCGGCGCGCGACGCGC 2159  
 DB 1813 GCGGATGAGTGGAGTCTTCCGTCGCTGCGGACCGGANTCAAGCGGCGCGCGACGCGC 1872  
 QY 2160 TCCTCATGCGCTCCGCTTCAAGCGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 2219  
 DB 1873 TCCTCATGCGCTCCGCTTCAAGCGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1932  
 QY 2220 GCAACGCTCCGCTGTCGACCGCGCTGAGCGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 2279  
 DB 1933 GCAACGCTCCGCTGTCGACCGCGCTGAGCGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1992

Qy 2280 CCTTCAACACCTCCGCGCTGAGTGCATTCGACCGCCGAGGCGCAAGCTGATCG 2339  
Db 1993 CGTTCAAGACGCGCGGCTCGGCTGAGCTTTGACCGCGCAGAGCAAAAGCTGATCG 2052  
Qy 2340 AGGCGCTCGGCACTGCTCCGCACTACCGGACCTTCAAGAGAGCTGAGGCGCTCC 2399  
Db 2053 AGGCGCTCGGCACTGCTCCGCACTACCGGACCTTCAAGAGAGCTGAGGCGCTCC 2112  
Qy 2400 AGGCGCGGCACTGCTCCGCACTACCGGAGAGCTGAGGAGCTTCAAGAGAGC 2459  
Db 2113 AGGCGCGGCACTGCTCCGCACTACCGGAGAGCTGAGGAGCTTCAAGAGAGC 2172  
Qy 2460 TCCCTTCAAGCGCAAGTCAAGCTGAGGAGCT 2493  
Db 2173 TCCCTTCAAGCGCAAGTCAAGTGAACCT 2206

RESULT 15  
AAZ50647/c  
ID AAZ50647 standard; cDNA; 1798 BP.  
AC AAZ50647;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
XX Corn starch synthase SSB fragment inserted in pSPB40.  
XX  
XX Starch synthase; SSB; starch fine structure; corn; transgenic plant;  
XX amylopectin; amylose polymerisation;  
XX non-granule bound starch synthase; non-GBSST; altered starch; food;  
XX paper; plastic; adhesive; ss.  
XX  
XX Zea mays.  
XX  
XX WO200006755-A2.  
XX  
XX 10-FEB-2000.  
XX  
XX 26-JUL-1999; 99WO-US016296.  
XX  
XX 28-JUL-1998; 98US-0094436P.  
XX  
XX (DUPLO) DU PONT DE NEMOURS & CO E. I.  
XX  
XX Broglie KE, Lightner JB;  
XX  
XX WPI; 2000-195311/17.  
XX  
XX Producing transgenic cereal crops with altered starch structure useful  
XX for preparing foodstuff, paper, plastic or adhesives, comprises  
XX transforming crops with chimeric sense or antisense gene construct  
XX encoding starch synthase.  
XX  
XX Claim 17; Page 55; 56pp; English.  
XX  
XX The present sequence is a corn starch synthase Ssb 1.8 kb insert in clone  
XX pSPB40. Purified pSPB40 is introduced into corn callus culture cells.  
XX Transgenic corn express altered starch structure. The starch fine  
XX structure derived from a grain of the cereal crop can be altered in the  
XX amylopectin fine structure, increased abundance of amylose. These  
XX modifications can be created by polymerisation of amylose. The  
XX (non-granule bound starch synthase) in transgenic plants. Altered  
XX starches are useful in foods, paper, plastics or adhesives  
XX  
XX Sequence 1798 BP; 389 A; 565 C; 466 G; 376 T; 0 U; 2 Other;  
XX

Query Match 43.8%; Score 1245.2; DB 3; Length 1798;  
Best Local Similarity 84.5%; Pred. No. 2.9e-213;  
Matches 1397; Conservative 2; Mismatches 255; Indels 0; Gaps 0;

Qy 640 CGCGCGCTGACGCCCGCTGTACAGAGACCTTTGGAGCTTCAAGAAATCATTTGGCT 699

Db 1696 CTCCTTCAAGTTAGCACTTAGTACAGAGGCGCACTTGGATTTCAAGAAATCATTTGGCT 1637  
Qy 900 TCGAGAGAGCGCTGAGAGCGCAAGAGTATGAGCTGGGCTGTTGCAAGATGAGCGGCTTCT 959  
Db 1636 TTGACAGAGCTTACAGAGAGAGAGATGATTCAGAGGTTGTCAGATGATGCTGCTTCT 1577  
Qy 960 TTGAACATCAGAGAGAGAGAGATTCAGAGCTTTGCGAGGAGAGAGAGAGAGAGAGAG 1019  
Db 1576 TTGAACATCAGAGAGAGAGAGATTCAGAGCTTTGCGAGGAGAGAGAGAGAGAGAGAG 1517  
Qy 1020 TCGTGTGCTGCTGATGATGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1079  
Db 1516 TCGTGTGCTGCTGATGATGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1457  
Qy 1080 GTGCTTTGCGCAAGGCTTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1139  
Db 1456 GAGCTTTACCAAGGCTTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1397  
Qy 1140 ATGGGAGACTATGAG 1199  
Db 1396 ATGGGAGACTATGAG 1337  
Qy 1200 AGGATATGAG 1259  
Db 1336 AGGATATGAG 1277  
Qy 1260 AGGCTGCTGCTTCCGAG 1319  
Db 1276 ATGCGCTTTTTCGAG 1217  
Qy 1320 TGAAGCGAGATTTTGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1379  
Db 1216 TGAAGCGAGATTTTGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1157  
Qy 1380 GCGGTGCTTCCCTATGAG 1439  
Db 1156 GTGATGTGCTAG 1097  
Qy 1440 TCTGCTGCTGCTATGAG 1439  
Db 1096 TCTGCTGCTGCTATGAG 1037  
Qy 1500 CCATATGAGATGATATGAG 1559  
Db 1036 CCATATGAGATGATATGAG 977  
Qy 1560 TCAACGAGTTGCTTGAAG 1619  
Db 976 ACATGAGCTTGTCTGAAG 917  
Qy 1620 AGCAGCGCAACTACTTCCGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1679  
Db 916 AGCAGCGCAACTACTTCCGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 857  
Qy 1680 CCGGCTTACTTGTGAG 1739  
Db 856 CCGGCTTACTTGTGAG 797  
Qy 1740 GGCAG 1799  
Db 796 GTTCTATGAG 737  
Qy 1800 CCGAGGTGAG 1859  
Db 736 CCGAGGTGAG 677  
Qy 1860 ACTCCGAG 1919  
Db 676 AGCTTGAAG 617  
Qy 1920 CGAGGTGAG 1979

Db	616	ACGACGTCGCCGTGCTTCGCGCTTCATCGCGCGCTTGATGACAGAAAGGCGGTGACATCA	557
Qy	1980	TGCGAGACGCATAGCCCTGGATCGTAGAGCCAGGACCGTGCAGCTGTCATGCTGGGACCG	2039
Db	556	TCCGGGACCGGATGCCGTGATCGCGGGGACGACGTGCAGCTGATGCTGGGACCG	497
Qy	2040	GCCGCAACGACTGAGAGCATGCTGGGCACTTTCAGCGGGAGCACACGACCAAGTGC	2099
Db	496	GCGCGCCGCACTGGAAACGAATGCTGACGACTTGAGCGCGGACATCCCAACAGTGC	437
Qy	2100	GCGGTGGGTGGGGTTCCTCGTGGCGCTTGCGGACCGGATCAAGCGGGCGCCGACGCG	2159
Db	436	GCGGTGGGTGGGGTTCCTCGTGGCGCTTGCGGACCGGATCAAGCGGGCGCCGACGCG	377
Qy	2160	TCCCATGACCTCCCGGTTGAGCGCCGTCGCGGTTGAACAAGCTTACGCCATGAGCTTACG	2219
Db	376	TGGTAGTGCCCTCCCGCTTGAGGCCCTGCGGGGCTGAACCAAGCTTACGCCATGAGCTTACG	317
Qy	2220	GCAACGTCGCCGTGCTGACACGCGTGGCGGGGTGAGGAGACACCGTACCGCGCTTGACCC	2279
Db	316	GCAACGTCGCCGTGCTGACACGCGTGGCGGGGTGAGGAGACACCGTACCGCGCTTGACCC	257
Qy	2280	CCTTCAACCACTCGGCGCTCGGGGTGAGCGTTTCAGACGCGCGCGAGGCGCACAGGTATCG	2339
Db	256	CGTTCAGGAGCGCGGGGTGAGGAGTTTTCACCGCGCGCGAGGCCAACAGGTATCG	197
Qy	2340	AGGCGCTCGGACATGCTCCGCACTTACCGGGACCTAACAGAGAGCTGAGGGGCTCC	2399
Db	196	AGGCGCTCAGGCACTGCTTCGACACGTAACGGAACTACAGAGAGAGCTGAGAAAGTCTCC	137
Qy	2400	AGGAGCGCGCATGTCCGAGGACTTTCAGCTGGAGCATGCCGCCAAGCTCTACAGAGAGC	2459
Db	136	AGGCGCGCGCATGTCCGAGGACTTTCAGCTGGAGCATGCCGCCAAGCTCTACAGAGAGC	77
Qy	2460	TCCCTCCTCAAGGCGCAAGTACAGAGTGAAGCCT	2493
Db	76	TCCCTCCTCAAGGCGCAAGTACAGAGTGAAGCCT	43

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OM nucleic - nucleic search, using sw model

Run on: February 22, 2004, 14:31:04 ; Search time 222 Seconds

(without alignments)  
7104.371 Million cell updates/sec

Title: US-10-018-418-3

Perfect score: 2842

Sequence: 1 gctgcaccaccctcgcctg.....aaaaaaaaaaaaaaaaaaaaa 2842

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/prodata/2/ina/Backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2392.2	84.2	2825	4 US-09-196-390-5	Sequence 5, Appl
2	1246	43.8	2248	4 US-09-345-214-20	Sequence 20, Appl
3	1246	43.8	2248	4 US-09-743-980-20	Sequence 20, Appl
4	1245.2	43.8	1798	4 US-09-345-214-16	Sequence 16, Appl
5	1245.2	43.8	2019	4 US-09-743-980-16	Sequence 16, Appl
6	1245.2	43.8	2019	4 US-09-345-214-15	Sequence 15, Appl
7	1245.2	43.8	2019	4 US-09-743-980-15	Sequence 15, Appl
8	1104.6	38.9	2007	3 US-08-572-951-2	Sequence 2, Appl
9	1104.6	38.9	2085	1 US-08-572-951-2	Sequence 2, Appl
10	1047.6	36.9	2097	3 US-08-572-951-3	Sequence 10, Appl
11	912.2	32.1	2380	1 US-08-572-951-3	Sequence 3, Appl
12	806.6	28.4	2348	4 US-09-388-743-25	Sequence 25, Appl
13	737.4	25.9	2348	4 US-09-388-743-5	Sequence 5, Appl
14	717.8	25.3	2793	3 US-08-836-567-7	Sequence 7, Appl
15	717.8	25.3	2793	3 US-09-606-304-7	Sequence 7, Appl
16	711.4	25.0	1926	3 US-08-836-567-5	Sequence 5, Appl
17	711.4	25.0	1926	3 US-09-606-304-5	Sequence 5, Appl
18	354.4	12.5	5058	4 US-09-889-595-1	Sequence 1, Appl
19	254.4	9.0	2542	3 US-08-941-445A-6	Sequence 6, Appl
20	250	8.8	2267	4 US-08-679-645-25	Sequence 25, Appl
21	248.4	8.7	1818	4 US-09-731-166-3	Sequence 3, Appl
22	215.4	7.6	2383	4 US-09-192-909-1	Sequence 1, Appl
23	215.4	7.6	2383	4 US-09-311-297-1	Sequence 1, Appl
24	213.8	7.5	1528	4 US-09-345-214-6	Sequence 6, Appl
25	213.8	7.5	1528	4 US-09-743-980-6	Sequence 6, Appl
26	213.8	7.5	2008	4 US-09-345-214-12	Sequence 12, Appl
27	213.8	7.5	2008	4 US-09-743-980-12	Sequence 12, Appl

28	213.8	7.5	2491	4 US-09-345-214-5	Sequence 5, Appl
29	213.8	7.5	2491	4 US-09-743-980-5	Sequence 5, Appl
30	205.4	7.2	1620	3 US-08-941-445A-20	Sequence 20, Appl
31	205.4	7.2	1752	3 US-08-941-445A-12	Sequence 12, Appl
32	196.2	6.9	2990	1 US-08-572-951-1	Sequence 1, Appl
33	195.8	6.9	2239	4 US-09-196-390-1	Sequence 9, Appl
34	188.8	6.6	2360	3 US-08-836-567-9	Sequence 9, Appl
35	188.8	6.6	2360	3 US-09-606-304-9	Sequence 9, Appl
36	171.4	6.0	1758	3 US-08-836-567-3	Sequence 3, Appl
37	171.4	6.0	1758	3 US-09-606-304-3	Sequence 3, Appl
38	143.4	5.0	2202	4 US-09-388-743-1	Sequence 1, Appl
39	138.6	4.9	1248	4 US-09-489-039A-3687	Sequence 3687, Ap
40	138.6	4.9	1536	4 US-09-489-039A-3682	Sequence 3682, Ap
41	127.8	4.5	2176	4 US-09-388-743-13	Sequence 13, Appl
42	125.4	4.4	2274	4 US-09-388-743-17	Sequence 17, Appl
43	123	4.3	1650	4 US-09-252-991A-8097	Sequence 8097, Ap
44	123	4.3	2145	4 US-09-352-991A-8205	Sequence 8205, Ap
45	105.6	3.7	1464	1 US-07-735-063-1	Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-09-196-390-5  
Sequence 5, Application US/09196390  
Patent No. 6307125  
GENERAL INFORMATION:  
APPLICANT: Block, Martina  
APPLICANT: Lorz, Horst  
APPLICANT: Luticke, Stephanie  
APPLICANT: Walter, Lemart  
APPLICANT: Kossemann, Jens  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES  
TITLE OF INVENTION: FROM WHEAT WHICH ARE INVOLVED IN STARCH  
TITLE OF INVENTION: SYNTHESIS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., C/O Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/196,390  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 196 21 588.9  
FILING DATE: 29-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 196 36 917.7  
FILING DATE: 11-SEP-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP97/02793  
FILING DATE: 28-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley, Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: AGREVO-9  
TELEPHONE: (212) 596-9090  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2825 base pairs



TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Trilecium aestivum L.  
STRAIN: cv. Florida  
TISSUE TYPE: ca. 21 d Caryopses  
IMMEDIATE SOURCE:  
LIBRARY: cDNA library in pluescript sk (-)  
CLONE: pTAS1  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 162..2559  
US-09-196-390-5

Query Match 84.2%; Score 2392.2; DB 4; Length 2825;  
Best Local Similarity 93.8%; Pred. No. 0;  
Matches 2613; Conservative 0; Mismatches 108; Indels 66; Gaps 9;

QY 2 CTGCCACCACTCTCCGCTGCGCGCTCTGCGCGAGAGACCAACCCGCGCATCTGCTCA 61  
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QY 62 TCGCCCGCCCGCATCCCGCGCGCGCGCATCTGCTGCGCGCTGCTGCGCGCTGCTGCTT 121  
DB 146 TCTCCCGCCCGCAT-----CAATGCTGCGCGCTGCTGCGCGCATCTCTTC 194  
QY 122 CTGCGCTGCGCTGCGCTGCGCTGCGCGAGATCAAGAGAGAGAGAGAGAGAGAGAGAG 181  
DB 195 CTGCGCTGCGCTGCGCTGCGCTGCGCGAGATCAAGAGAGAGAGAGAGAGAGAGAGAG 254  
QY 182 CCAACCCACGCGCGCGCGCGCGAGCTGCACTGCGCGCTGCGCGCGCGCGCGCGCGCT 241  
DB 255 CCAACCCACGCGCGCGCGCGCGAGCTGCACTGCGCGCTGCGCGCGCGCGCGCGCGCT 314  
QY 242 CCGGAG 301  
DB 315 CCGGAG 374  
QY 315 CCGGAG 421  
DB 302 GCGCGCTGCGCGAG 361  
QY 375 GCGCGCTGCGTAG 434  
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QY 435 CCGAG 494  
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QY 495 CCGGAG 554  
DB 482 GAG 541  
QY 555 GAG 614  
DB 542 CCGGCGCGCGCATCTGCTGCACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 601  
QY 615 CCGGCGCGCGCATCTGCTGCACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 674  
DB 602 GTGCGCTGCGCGCGAG 661  
QY 675 GTGCGCTGCGCGCGAG 734  
DB 662 TCCATCAGTGAACAAG 721  
QY 735 TCCATCAGTGAACAAG 794  
DB 722 GAGTCAAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 781  
QY 795 GAGTCAAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 854

QY 782 CCTGAAGTGAAG 841  
DB 855 CAAGAAGTGAAG 914  
QY 842 CCGCGCTGAG 901  
DB 915 CCGCGCTGAG 974  
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DB 1695 CAGGCGCAACTTCTGCGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1754  
QY 1682 GAGTACCTGTGAG 1741  
DB 1755 GAGTACCTGTGAG 1814  
QY 1742 CAG 1801  
DB 1815 CAG 1874  
QY 1802 GAGGTGAG 1861  
DB 1875 GAGGTGAG 1934



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; SEQ ID NO 20
; LENGTH: 2248
; TYPE: DNA
; ORGANISM: Zea mays
US-09-743-980-20

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1393 GCGGCTACCTGTGGAGCTCAAGACGGTGGAGGGCGGCTGGGGCTTCAAGCATCATAC 1452
1740 GCGGATACCTGTGGAGCTCAAGACGGTGGAGGGCGGCTGGGGCTTCAAGCATCATAC 1799
1453 GTTCTAACGACTGGAGATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1512
1800 CCGAGTGGAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 1859
1513 CCAAGTGGAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 1572
1860 ACTCCGGAACGGGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1919
1573 AGGCTGAAAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1632
1920 CCGAGTGGAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 1979
1633 ACAGCTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 1692
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1693 TCGGAGAGCGGAGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 1752
2040 GCGGAGAGCGGAGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 2099
1753 GCGGAGAGCGGAGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 1812
2100 GCGGAGAGCGGAGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 2159
1813 GCGGAGAGCGGAGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 1872
2160 TCTCATGCTCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 2219
1873 TGGTGAATGCTCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 1932
2220 GCGGAGAGCGGAGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 2279
1933 GCGGAGAGCGGAGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 1992
2280 CTTTCAACCACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 2339
1993 GGTTCAGAGAGCGGAGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 2052
2340 AGGAGTGGAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 2399
2053 AGGAGTGGAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 2112
2400 AGGAGTGGAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 2459
2113 AGGAGTGGAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 2172
2460 TCTTCTCAAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 2493
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; SEQ ID NO 20
; LENGTH: 2248
; TYPE: DNA
; ORGANISM: Zea mays
US-09-743-980-20

Query Match 43.8%; Score 1246; DB 4; Length 2248;
Best Local Similarity 84.6%; Pred. No. 3,6e-242;
Matches 1399; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

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553 CTCCTAACGATGAGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 612
900 TCGAGAGCGGAGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 959
613 TTGACAGGCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 672
960 TTGACATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1019
673 TTGACATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 732
1020 TCGTGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1079
733 TCGTGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 792
1080 GTGCTTGGCCAAAGCTTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1139
793 GAGCTTACCAAGGCTTACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 852
1140 ATGGGAGCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1199
853 ATGGGAGCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 912
1200 AGGATGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1259
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1260 AGGCTCTCTCTTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1319
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1440 TCTTGTCTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1499
1153 TCTTGTCTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1212
1500 CCAATTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1559
1213 CCGTCTCTCTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1272
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1273 ACATGAGCTTGGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 1332
1620 AGGAGGAGGAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 1679
1333 AGGAGGAGGAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 1392
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1740 GCGGATACCTGTGGAGCTCAAGACGGTGGAGGGCGGCTGGGGCTTCAAGCATCATAC 1799
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DB	Sequence	Score	DB	Length
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Db	616 AACACGCGCGCTGCTGCTTCAATGACCGCGCTGAGTGAACAAAGGGGCTGACATCA	557		
Qy	1980 TCGCGAGCGCATGCGCTGATCGTAGACCAAGACGTGACCTGATCATGCTGGACCG	2039		
Db	556 TCGGAGACGGATGCGCTGATGCGCGGAGGACGTGACGCTGATGCTGGACCG	497		
Qy	2040 GCCGCCACGACCTTGAAGACATGCTGGGCACTTCAAGCGGGAGACACACGAAGA	2099		
Db	496 GGCACGCGGACCTGAACGAACTGTGAGACCTTGGAGCGGAGACATCCAAACA	437		
Qy	2100 GCGGAGGTGGGCTTCTCCGTGCGCCTGAGCGACCGAATCACGGCGGGCGCCGAC	2159		
Db	436 GCGGTGGGTGCGATTCCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	377		
Qy	2160 TCCCTCAGCCCTCCCGGCTTGAAGCGCGGCTTGAACCACTTTAAGCAGTGGCTAC	2219		
Db	376 TGTGATGCTCTCCCGCTTGAAGCTGAGCTGAGCTGAACCAAGCTTACGATGCA	317		
Qy	2220 GCACCGTCCCGTGTGTGACCGCGTGTGCGCGGGGTGAGAGACACCGTGCCTTGAC	2279		
Db	316 GCACCGTCCCGTGTGTGACCGCGTGTGCGCGGGGTGAGAGACACCGTGCCTTGAC	257		
Qy	2280 CCTTCAACCACTCCGGGCTGCGGTGAGCGTTGACCGGCGGAGGACCAAGTGTG	2339		
Db	256 CTTTCAACCACTCCGGGCTGCGGTGAGCGTTTGAACCGGCGGAGGACCAAGTGTG	197		
Qy	2340 AGCGCGTGGGCACTGCTCCGCACTACCGGAGCTACAGAGAGCTGAGGGGCTCC	2399		
Db	196 AGCGCGTGGGCACTGCTCCGCACTACCGGAGCTACAGAGAGCTGAGGGGCTCC	137		
Qy	2400 AGGAGCGGGGATGTGCGAGGACTTCACTGAGGAGATGCGCGCAAGCTTACAGAGAG	2459		
Db	136 AGGAGCGGGGATGTGCGAGGACTTCACTGAGGAGATGCGCGCAAGCTTACAGAGAG	77		
Qy	2450 TCTCTCTCAAGGCCAAGTACCAAGTGTGACGCT	2493		
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RESULT 5				
US-09-743-980-16/c				
Sequence 16, Application US/09743980				
Patent No. 657008				
GENERAL INFORMATION:				
APPLICANT: E. I. du Pont de Nemours and Company				
TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE				
FILE REFERENCE: BB-1147-A				
CURRENT APPLICATION NUMBER: US/09/743,980				
CURRENT FILING DATE: 2001-05-14				
PRIOR APPLICATION NUMBER: 060/094,436				
PRIOR FILING DATE: 1998-07-28				
NUMBER OF SEQ ID NOS: 20				
SOFTWARE: Microsoft Office 97				
SEQ ID NO 16				
LENGTH: 1798				
TYPE: DNA				
ORGANISM: Zea mays				
US-09-743-980-16				
Query Match 43.8%; Score 1245.2; DB 4; Length 1798;				
Best Local Similarity 84.5%; Pred. No. 4,9e-242;				
Matches 1397; Conservative 2; Mismatches 255; Indels 0; Gaps 0;				
Qy	840 CGCGGCTCAGCGCCCGCTGATCAAGAGACCTTTGGAGCTTCAAGAAATACATTGCT	899		
Db	1696 CTCTCAAGTGAAGCATTAGTACAGAGAGCCACTTGGATTTCAGAAATACATCGGT	1637		
Qy	900 TCGAGAGCCCGTGAAGGCCAAGATGATGCTGGGCTTTCAGATATATGCGGGCTCT	959		

Db	1636	TTGACGAGCCTGACGAGAGGAAAGATGATTCGAGGGTTGGTCCAGATGATGCTGGTCTT	1577
Qy	960	TTGAAACATCACAGAAACCATGATTCGGACCTTTGGCAGGGAGAAACCTCATGAACCGTGG	1019
Db	1576	TTGAAACATTATGGGGACAATGATCTCGGGCCCTTTGGCCGGGAGAAATGTTATGAACGTGA	1517
Qy	1020	TGCGTGGGCGTGTGATGATGTCCTCCGTGGTCAAAACAGGTGCTTTGGAGATGTTCCGG	1079
Db	1516	TCGTGGTGGTGTGCTGATGATGTCCTCCATGGTGCAAAACAGTGGTCTTGGAGATGTTGTGG	1457
Qy	1080	GTCGCTTTGGCCCAAGCGCTTTGGCGAAGAGAGACATGCTGTATAGTTAGTTGGTACCAAGGT	1139
Db	1456	GAGCTTTTACCCAAAGGCTTTTAGCCAGAAAGAGACATGCTGTATAGTTAGTTGGTACCAAGGT	1397
Qy	1140	ATGGGGACATATGAGAAAGCCTACAGATGTGCGAGTCCGAAATATCTACAGAGCTGTGAC	1199
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Qy	1200	AGGATATGAAAGTGAATATTTTCGATGCTTATATCGATGAGAGTGAATTTTGGTGTCAATGG	1259
Db	1336	AGGACCTTAGAAGTAATATTTTCATGACATTTATGATGGAGTGCACCTTGTGTATTGG	1277
Qy	1260	ACGCTCTCTCTTCCGACACCGCGCAGGAGACATTTATGGGGCAGACAGACAGAAATTA	1319
Db	1276	ATGCCCTCTTTTCCGGCACCGTCAAAATGACATATATGGGGAGATGAGCAGAGAAATCA	1217
Qy	1320	TGAAGCGCAGATTTTGTTCGCAAGGCGCTGTCCAGAGTTCCTTGGACGTTCCATGCG	1379
Db	1216	TGAAGCCCATGAAATTTGTTTTGCAAGGTGTCTGTGAGTTCCTTGGACGTTCCATGCG	1157
Qy	1380	GCGGTGTCCCTTATGGGGATGAAATCTGTGTTTATTTGCAATGATTTGGCAACACGCGAC	1439
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Qy	1560	TCAACGAGTTGCCGAGACATCACTGGAACCTTCAACCTGATACACCCGTGGGTGGT	1619
Db	976	ACATGACCTTGCCTGACACATCACTTCACTTTGAGCTGTAGACATCCGTGGTGGGCG	917
Qy	1620	AGCAGCGCAACTACTTGCCTGGCGCGGCTGTGAAGATGCGGACAGGTGTGTGTGTAGCC	1679
Db	916	AGCAGCGCAACTACTTGTCCGCGGGGTGTGAAGATGCGGACCGGATGGTGACTGTGCAGCC	857
Qy	1680	CCGGGTACCTGTGGGAGCTCAAGAACGGGTGAAGGGCGGTGGGGCTTCAACACATCATATAC	1739
Db	856	GCGGCTTACTGTGGGAGCTGAAGACGTGAAGACGGGTGGGGCTTCAACACATCATATCC	797
Qy	1740	GCGAGAACGACTGGAAGACCCGCGGCACTGTCAACCGCATGACAACTTCTCCCTGGGAGCGTGG	1799
Db	796	GTTCTTAAGACTGGAAGATCAATGACATCTGGAACGGCATGACACACAGAGTGAAC	737
Qy	1800	CCGAGTGAAGCTTCCACCTCAAGTGGAGCGCTACACCACTTCTCCCTGGGAGCGTGG	1859
Db	736	CCAAAGTGAAGTGAACCTTCCGGGTGGACGGCTTACCACTTCTCCCTGGAGACATCG	677
Qy	1860	ACTCCGGCAAGCGGCAATGTGCAGAGAGCGCCCTTGCAACCGCACTGGGCTCTGAGGTCCGGG	1919
Db	676	ACGCTGGAAGAGCGGCAATGTGCAGAGAGCGCCCTTGCAACCGGAACTGGGCTCTGGAAGTGGCG	617
Qy	1920	CCGAGTGAAGCTGTGCTCGGCTTCACTCGGCGCGCTGAGCGGCGCAGAGAGCGCTGAGATCA	1979
Db	616	ACGAGCTGCGCTGTCTCGGCTTCACTCGGCGCGCTGAGCGGCTGAGCGGCGCTGAGATCA	557
Qy	1980	TGCGGAGCGCATGCTCTGATCTGTAGACCAAGATGTGCACTGGTCACTGCTGGCAACG	2039



Db 556 TCGGGAGCGGATGCCGTGATCCGGGAGAGACCTGACGCTGTGATGTCGGACCG 497  
Qy 2040 GCCGCGACGACCTGAGAGCATGTGCGGACCTTCCAGCGGAGACCAACGAACTGC 2099  
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Qy 2160 TCCATGACCTCCCGGTTTCCAGCGGCTGCGGATGAAACCACTTTACGCCATGCTTACG 2219  
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## RESULT 6

US-09-345-214-15  
Sequence 15, Application US/09345214  
Patent No. 6392120  
GENERAL INFORMATION:  
APPLICANT: Lightner, Jonathan E.  
TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE  
FILE REFERENCE: BB-1147  
CURRENT APPLICATION NUMBER: US/09/345,214  
EARLIER FILING DATE: 1999-06-30  
EARLIER APPLICATION NUMBER: 060/094,436  
EARLIER FILING DATE: 1998-07-28  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 15  
LENGTH: 2019  
TYPE: DNA  
ORGANISM: Zea mays  
US-09-345-214-15

Query Match 43.8%; Score 1245.2; DB 4; Length 2019;  
Best Local Similarity 84.5%; Pred. No. 56-242;  
Matches 1397; Conservative 2; Mismatches 255; Indels 0; Gaps 0;  
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Db 109 CTCCTACAGTTAGCATTAATGACAGAGGCACTTGGGATTTCAAGAAATACATCGATT 168  
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Qy 960 TTGACATCAACGAGACATGATTCGCGACCTTTGGGAGGAGAGACGTCATGAACGTGG 1019  
Db 229 TTGACATTAATGGGAGCAATGATTCGCGGCTTTGGGAGGAGATGTTATGAACGTGA 288

Qy 1020 TCGTGTGCTGCTGAAATGTTCTCCCTGTGTGCAAAAGAGTGTCTTGGAGATGTCGCG 1079  
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Qy 1080 GTGCTTTGCCAAGGCTTTGGCGAAGAGAGACATGCTGTTATGTTGTGTGTACCAAGCT 1139  
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Db 1729 TCCCTCAAGGCGCAAGTACCAAGTGGTGAAGCT 1762

RESULT 7  
US-09-743-980-15  
; Sequence 15, Application US/09743980  
; Patent No. 6570008  
; GENERAL INFORMATION:  
; APPLICANT: E. I. du Pont de Nemours and Company  
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE  
; FILE REFERENCE: BB-1147-A  
; CURRENT APPLICATION NUMBER: US/09/743,980  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 060/094,436  
; PRIOR FILING DATE: 1998-07-28  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 15  
; LENGTH: 2019  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-743-980-15

Query Match 43.8%; Score 1245.2; DB 4; Length 2019;  
Best Local Similarity 84.5%; Pred. No. 56242;  
Matches 1397; Conservative 2; Mismatches 255; Indels 0; Gaps 0;

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 Db 1729 TCCTTCTCAAGGCGCAAGTACCAATGTGTGAACCT 1762

## RESULT 8

US-08-941-445A-8  
 Sequence 8 Application US/08941445A  
 Patent No. 6107060

## GENERAL INFORMATION:

APPLICANT: Keeling, Peter  
 APPLICANT: Guan, Haining  
 TITLE OF INVENTION: Starch Encapsulation  
 NUMBER OF SEQUENCES: 37  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
 STREET: 5370 Manhattan Circle  
 CITY: Boulder  
 STATE: CO  
 COUNTRY: US  
 ZIP: 80303

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/941,445A  
 FILING DATE: 30-SEP-1997  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/026,855  
 FILING DATE: 30-SEP-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Winner, Ellen P  
 REGISTRATION NUMBER: 28,547  
 REFERENCE/DOCKET NUMBER: 89-97  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 499-8080  
 TELEFAX: (303) 499-8089  
 INFORMATION FOR SEQ. ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2007 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: not relevant  
 MOLECULE TYPE: cDNA to mRNA  
 HYPOTHEICAL: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Zea mays

FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..2007  
 US-08-941-445A-8

Query Match 38.9%; Score 1104.6; DB 3; Length 2007;  
 Best Local Similarity 81.7%; Pred. No. 1,1e-213;  
 Matches 1340; Conservative 0; Mismatches 289; Indels 12; Gaps 5;

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 Db 1388 TGAAGTCCGAG 1447

Mon Feb 23 11:51:11 2004

us-10-018-418-3.rn1

Page 10

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QY 1917 GCGCCGACCTGCGCGCTGCTGGCTTATCGAGCGCCCTGAGCGGACGAAAGGCGTGAG 1976
Db 1448 GCGACGACGCGCGCTGCTGGCTTATCGAGCGCTGAGACGAGACGCGCTGAGCA 1507
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Db 1985 ACGTCTCTCTCAAGTACCAAGT 2005

RESULT 9
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/ Sequence 2, Application US/08572951
/ Patent No. 5824790
/ GENERAL INFORMATION:
/ APPLICANT: KEELING, PETER L.
/ APPLICANT: KNIGHT, MARY E.
/ APPLICANT: GUAN, HANPING
/ TITLE OF INVENTION: MODIFICATION OF STARCH
/ TITLE OF INVENTION: SYNTHESIS IN PLANTS
/ NUMBER OF SEQUENCES: 41
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: CUSHMAN DAREY & CUSHMAN
/ ADDRESSEE: Intellectual Property Group of
/ ADDRESSEE: Pillsbury Madison & Sutro LLP
/ STREET: 1100 New York Avenue, N.W.
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3918
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/572,951
/ FILING DATE: 15-DEC-1995
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/346,602
/ FILING DATE: 29-NOV-1994
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RESULT 10
US-08-941-445A-10
; Sequence 10, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Heping
; TITLE OF INVENTION: Starch Encapsulation

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; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Wimer and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wimer, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2097 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2097
; US-08-941-445A-10
;
Query Match 35.9%; Score 1047.6; DB 3; Length 2097;
Best Local Similarity 78.7%; Pred. No. 3.3e-202;
Matches 1264; Conservative 0; Mismatches 339; Indels 3; Gaps 1;

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QY 886 GAATATCATTTGCTTGAAGAGCCCGTGAAGCCAAAGATGATGAGCTGGGCTGTTCAGA 945
DB 492 GAAATCATTAAGGATGCTGAACCGGTGATGCTAAGGCTGATGACAGCTCCGGCTACAGA 551
QY 946 TGATGGG---GCTCTTTGAACATACAGAACATATTCGGACCTTTGGCGAGGGA 1002
DB 552 TGGGGGGGGAAGTCTCTTATGACAGGAGATATGAACCTGGCCCTTTGGCTGAGCC 611
QY 1003 GAAGTCATGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1062
DB 612 TAATGATGATGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 671
QY 1063 TCTTGAAGATGTGCGCGCTGCTTTCGCGCAAGCTTTGGGAGAGAGAGAGAGAGAGAGT 1122
DB 672 CTTTGAAGATGTGCGCGCTGCTTTCGCGCAAGCTTTGGGAGAGAGAGAGAGAGAGAGT 731
QY 1123 GATTGTGATCAAGGATATGGGAGATATGAGAGAGCTACGATGTGCGAGTCCGAATAA 1182
DB 732 GGTGATGATCAAGATATGAGAGAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 791
QY 1183 CTACAGAGCTGTGAGACAGAGATATGAGAGAGTGAATTTTCATGCTTATATGATGAGT 1242
DB 792 TTACAAGTGTGCTGAGACAGAGATATGAGAGAGTGAATTTTCATGCTTATATGATGAGT 851
QY 1243 TGATTTTGTGATTTGATGAGAGCTCTCTTCGAGACAGCGAGAGAGAGAGAGAGAGAGAGT 1302
DB 852 TGATTTTGTGATTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 911

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QY	QY	QY	QY
2383	GAGCTGGAGGGGGCTCCAGGAGGGCGGCAATGTGCAGAGATTACAGCTGGGAGCATGCGC	2442	
1992	GAGCTGGCGCGCTCCAGGAGGGCGCGGCAATGTGCAGAGATTACAGCTGGGAGCATGCGC	2051	
2443	GAGCTTACAGGAGAGCTCTCTCCAGGAGGGCAATACAGAGTGTGA	2488	
2052	CGTCTGTATAGGAGACGCTCTCTCCAGGAGGGCAATACAGAGTGTGA	2097	

US-08-572-951-3  
; Sequence 3, Application US/08572951

; Patent No. 5824790

GENERAL INFORMATION:  
APPLICANT: KEELING, PETER L.

APPLICANT: KNIGHT, MARY E.  
APPLICANT: GUAN, HANPING

TITLE OF INVENTION:	MODIFICATION OF STARCH
TITLE OF INVENTION:	SYNTHESIS IN PLANTS

NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:

ADDRESS: CUSHMAN DARBY & CUSHMAN  
Intellectual Property Group of

ADDRESSES: Pillsbury Madison & Sutor LLP  
100 New York Avenue N W  
ADDRESSES:

STREET: 1100 New  
CITY: Washington

```
STATE: DC
COUNTRY: USA
```

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;      ZIP: 20005-3918
;      COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/572,951

FILING DATE: 15-DEC-1995  
CLASSIFICATION: 800

PRIOR APPLICATION DATA:  
PRIORITY NUMBER: 08/346 602

APPLICATION NUMBER: 08/570,002  
FILING DATE: 29-NOV-1994  
CLASSIFICATION: 000

```

; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
;

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APPLICATION NUMBER: 08/263,921  
FILING DATE: 21-JUN-1994

CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:

NAME: Paul N. Kokulis  
REGISTRATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 222957/1.02.15C  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS.

SEQUENCE CTTGCTTATCAAGACCG;  
LENGTH: 2380 base pairs  
;

STRANDEDNESS: both

TOPOLOGY: linear  
MOLECULE TYPE: cDNA

US-08-572-951-3

Query Match 32.1%; Score 912.2; DB 1; Length 2380;

Best Local Similarity 53.4%; Pred. No. 6.6e-1/5;  
Matches 858; Conservative 291; Mismatches 454; Indels 3; Gaps 1

888 AATACATTGGCTTCGAGAGCCCCGTGAGGCCAAGATGATGCTGGCTGTTGAGATG 947

Db 551 ARMSNATHGSNATHGCGARCCNGTGTGAYCGMAARCGNGAYGCGNGCNCNGCNAAGAYG 610

948 ATGCGGGCTTCTTTGAACATCACC--AGAACCATGATTCGGACCTTTGGCAGGGGAGA 100

611 CMCNCGTSSNCGCCNCTAAYGAYMGNGARGA YAAAGARCNGNGCCNCTINGCNGNCNA 670

[illegible]

QY	2085	ACCAACAACAAGATGCGCGGATGGAGTTCCTCCGCGCCCTCGCGGCACCGATCAAGG	2144
Db	1751	AYMSNGBYAARGTINMGNCNTGGGTGNGTNTTWSNNGNCNNTYNGCNCAVMGNATHACNG	1810
QY	2145	CGGGCGCCGACGCGCTCTCATGCCCTCCCGGTTTGAAGCCGTGGCGGTTGAACAAGTTT	2204
Db	1811	CNNGNGCNGAATHTHTYTNATGCMMSNMNGNTTYGARCNTGTGGYNTNAAACARYNT	1870
QY	2205	ACGECATGCGCTTACGGACAACGTCCTCCCGTCGTGACGCGCCTCGGCGGGGTAGAGGACACCG	2264
Db	1871	AYGCAATGGCNTAAGNAACNGTNCNNTGNTNCAYGCGNTGNGGNYTNMGNAIACNG	1930
QY	2265	TGCCGCGGTTGCAGACCCCTTCAACACACTCCGAGCTCGGATGGAGCTTGCACGCGCCAGG	2324
Db	1931	TNGCNCCNTTYGACNTTYTAAYAYACNNGNNTNGNTGACNTTYGATMGNGCNGARG	1990
QY	2325	CGACAAGCTGATCGAGCGCGCTCGGAGCATGTCCTCGGACCTTACCGGGACTACAAGAGA	2384
Db	1991	CNAAYMGNAATGATGAYGCNVTYTNMSNCAITGYTNAACNATAVMGNAAATAYAAARGAR	2050
QY	2385	GCTGGAGGGGCTCTCAGAGAGCGCGGCATGTTCGACGACCTTCACTGGGAGGATGCGGCCCA	2444
Db	2051	SNTGCGMGNCNTGTMGNGCMNMGNGNATGGCNGARGAYTNTWSNTGGGAACAYCGNGCG	2110
QY	2445	AGCTCTACGAGACGTCCTCTCAAGGCAAGTACCAATGAGTGGTGAAC	2490
Db	2111	TNYTNTAYAGARGAYGINTYTGNTNARGNAAATYCACTGGTTRGC	2156

RESULT 12  
US-09-388-743-25  
; Sequence 25, Application US/09388743

```

1 / Patent No. 6423886
2 /
3 / GENERAL INFORMATION:
4 /
5 / APPLICANT: Singletary, George
6 /
7 / APPLICANT: Zhou, Ian
8 /
9 / TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and Their
10 /
11 / TITLE OF INVENTION: Use in the Production of New Starches
12 /
13 / FILE REFERENCE: 1144
14 /
15 / CURRENT APPLICATION NUMBER: US/09/388,743
16 /
17 / CURRENT FILING DATE: 1999-09-02
18 /
19 / NUMBER OF SEQ ID NOS: 28
20 /
21 / SOFTWARE: PasteSeq for Windows Version 3.0
22 /
23 / SEQ ID NO 25
24 /
25 / LENGTH: 2418
26 /
27 / TYPE: DNA
28 /
29 / ORGANISM: Typha latifolia
30 /
31 / FEATURE:
32 /
33 / NAME/KEY: CDS
34 /
35 / LOCATION: (1)...(2418)
36 /
37 / US-09-388-743-25

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Query Match	28.4%	Score 805.6;	DB 4	Length 2418;
Best Local Similarity	70.7%	Pred. No. 1,2e-153;		
Matches 1073; Conservative	0;	Mismatches 444;	Indels 0;	Gaps 0;

Qy	972	AAACCAAGATTCGGACCTTTGGCAGGGGGAACGATGAAACGTGGTCGCGAGCTG	1033
Db	638	AAAAAGAGGTTCTCTTCTTTGGCTGGGGCAAAATGTCATGAACATCAATAGTAGTGGTG	697
Qy	1032	CTGAATGTTCTCCCTGGTGC AAAA CAGGTGGTCTTTGAGATGTTGCCGCTGTTGCCA	1099
Db	698	CAGATGTCCTCTTGGTCCAAAA CAGGTGGGCTTGGAGATGTTGCAGAGAGCATGGCGA	757
Qy	1092	AAGCTTTGGCGAAGAGAGACATCGTGTATAGTGTGATGC CAAGTATGGGAGCTATG	1155
Db	758	AAGCTTTGGCGAAGAGAGACATAGGTCATAGTGTGTGGCACCAAGATATGAAACTATG	817
Qy	1152	AGGAAGCCATCGATGTCGAGTCCGAAAATACTACAAGCTGCTGGACAGATATGAGAG	1211
Db	818	CTGAACCCCAAGATATAGGAGTCCGCAATACTACAAGTTCATGGGACAGGATATGAGAG	877
Qy	1212	TGAATATTTCCATGCTTATATCGATGAGAGTTGATTTTGTTGTTATGACGCTCCTCTCT	1271



Db 878 TAACTTATTTTCATGCTTATATGACGCTGATGATTTTGTATTTTATGATAGTCCAGACT 937  
 Qy 1272 TCCGACACCGCCAGAGAGACATTTATGGGGGACAGACAGAAATTTATGAAAGCCATGA 1331  
 Db 938 TCCGTCAACCGGGGAAATCGTATTTATGAGGAAACCAGTGAATCTTAAACCTATGA 997  
 Qy 1332 TTTTGTCTGAAAGCGCGCTGTGAGGTTCTTGACGCTTCCATGCGGCGGTCTCCCTT 1391  
 Db 998 TTTTGTCTGAAAGCGCGCTGTGAGGTTCTTGACGCTTCCATGCGGCGGTCTCTCTT 1057  
 Qy 1392 ATGGGATGGAATCTGTGTTTATTTGCAATGATTTGCAACAGGCACTCTCTCTCTCT 1451  
 Db 1058 ATGGAGATGGAATTTGGCTTTTCAATCAAGATGATGCGATACGCTCTCTCTCTCTT 1117  
 Qy 1452 ATCTGAAGCATTTTACAGGAGCAATGTTTGAATGACGTACACTCGGTCATTAATGCTGA 1511  
 Db 1118 ATCTGAAGCATTTTATTCGTGACAAATGCTGATGAATATGCTCGGTCGTTCTGCTTAA 1177  
 Qy 1512 TACATTAATCATGCGCACACGAGCGCTGCGCCAGTGAATGATTCCTTCACGAGTTGC 1571  
 Db 1178 TACACAAATAGCCACACGAGGTGCTGCTGATGATGATTTCAATTTGTGGGCTTGC 1237  
 Qy 1572 CTGACATTAATCTGAAACATTTCACTGATGACACCCCGGTGGTGTGAGAGCCCACT 1631  
 Db 1238 CGGATCACTACTTGGACCTTTTCAGATTGTATGACCCCGTGGAGGTGAAACCTCAATA 1297  
 Qy 1632 ACTTGCCGCGCGCTGGAAGATGGCGGACAGGTTGTCTGTGTGAGAGCCCGGATACCTGT 1691  
 Db 1298 TTTTGTCTGCTGCGCTGGAAGACTGCTGACCGAGGTGTATCTGTAGCATGTTATGCAT 1357  
 Qy 1692 GGGAGCTCAAGCGGTGAGGGCGGCTGGGGCTTACAGACATCATAGGAGAGACACT 1751  
 Db 1358 GGGAGCTCAAGACATCAAGAGGTGTGGGGCTTACAGAAATTAATTAATGAATTAATCT 1417  
 Qy 1752 GGAAGACCGCGGCGATCTGCAACGCGCATGCAACATGATGATGAAACCCCGAGGTGACG 1811  
 Db 1418 GGAATTTCAAGGTATTTGAAATGAGCATTTGATGCAAGAGATGAGAGCCCGAATTTGATG 1477  
 Qy 1812 TCCACTTCAAGTGGACGCGCTTACCAACTTCTCCCTGGGGACGCTGACATCCGCAAGC 1871  
 Db 1478 TCCACTTCAAGTGGACGCGCTTACCAACTTCTCCCTGGGGACGCTGACATCCGCAAGC 1537  
 Qy 1872 GGCAGTGCAGAGAGCGCTGACGCGGAGCTGGGCTGAGGTCCGCGCCAGCGTCCGC 1931  
 Db 1538 CAGTATGTAAGGCTGTTTGCACGAGAGGTGCGCTGCTGTGTGTAATATGACCA 1597  
 Qy 1932 TGTCTGGCTTCAATCGGCGCTGACGCGGAGAGAGGGCGTGGAGATCATCGGACGCA 1991  
 Db 1598 TCAATGCAATTTGAGAGGTTAGACCAACAGAAAGGCGTGCATCTCATTTGCCAGGCA 1657  
 Qy 1992 TGCCCTGAGTCCGAGACCGAGAGCTGACGCTGATGCTGAGGCAACCGGCGCCAGAC 2051  
 Db 1658 TGCTTGGATGTCAGTCAATGATGTTCAAGTATGATCTTTAGGCAAGGGAGGCAAGAC 1717  
 Qy 2052 TGGAGAGCATGCTGCGGCACTTTCAGAGCGGAGACCAACAGCAAGGTGGCGGGTGGTGG 2111  
 Db 1718 TTAGAATTTACTGAGGAACTTTGAGGCTCAACAGGAGCAAAAGTTAGAGCATGAGTGG 1777  
 Qy 2112 GGTTCCTCGGCGCTGCGGCAACCGGATCAACGCGGCGGCGGCGGCTCATGCGCT 2171  
 Db 1778 CATTTTCAGTAAGATGAGCGCATGATTTACAGAGGTGCGACATCTCTCATGATGCTT 1837  
 Qy 2172 CCGGATTCAGCGCGTGGCGGTTGAACCAAGTTTACGCAATGCTTACGCAAGCGTCCCG 2231  
 Db 1838 CAGAGTTTGAAGCATGAGGATGAAACAGCTTTACCAATGATGATGAAACATTTCCAG 1897  
 Qy 2232 TCGTGCACGCGCTCGGGGGGTGAGGAGCAACGCTGCGCGCTTCAACCAACT 2291  
 Db 1898 TGGTGCATGCTGTGGGGGCTTGAAGATTAAGTATCAATTTGATCTTTTCAAGAGAT 1957  
 Qy 2292 CCGGCTTCGGGTGAGCTTGAACCGCGCGGAGGCGCAAGCTGATGAGAGCGCTCGGCG 2351

Db 1958 CTGCTCTGTTGGACCTTCGACAGGCGAGAGGAGGAAAGTGAATCATGATGATA 2017  
 Qy 2352 ACTGCTCCGACCTTACCGGAGTACTACAGAGAGCTGAGGCGCTCCAGAGCGGCA 2411  
 Db 2018 ACTGCTGAATACATCTGGAATTTACAGAGCACTTGGAGGGCTTCAACAGAGGGA 2077  
 Qy 2412 TGTGCGAGACTTCACTGCGGAGCATGCGCCAGCTCTACAGAGAGCTCTCTCAAG 2471  
 Db 2078 TGATCAAGATCTTACGCTGGGATATGCTGCTCAGCAATGAGAGATGCTTGTGCG 2137  
 Qy 2472 CCAAGTACAGTGGTGA 2488  
 Db 2138 CCAAGTACCAATGGTGA 2154  
 RESULT 13  
 US-09-388-743-5  
 ; Sequence 5, Application US/09388743  
 ; Patent No. 6423886  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Singletary, George  
 ; TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and their  
 ; FILE REFERENCE: 1144  
 ; CURRENT APPLICATION NUMBER: US/09/388,743  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 5  
 ; LENGTH: 2348  
 ; TYPE: DNA  
 ; ORGANISM: Curcuma zedoaria  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (36)...(2105)  
 ; US-09-388-743-5  
 Query Match 25.9%; Score 737.4; DB 4; Length 2348;  
 Best Local Similarity 67.9%; Pred. No. 1.1e-139;  
 Matches 1029; Conservative 0; Mismatches 486; Indels 0; Gaps 0;  
 Qy 974 AACCATGATTCGCGACCTTTGGCAGGGAGAACTCATGAAGTGTGCTGGCTGCT 1033  
 Db 594 AATCTGAACCTCTCTCTTGTGCTGCTCCAAATGATATAATATCATATTGTAAGTGA 653  
 Qy 1034 GAATGTTCTCCCTGTGCAAAAACAGGTGCTTGTGAGATGTTGCCGCTTTGCCAAG 1093  
 Db 654 GAATGTCACCAATGCTTAAACAGGTGGGCTTGAAGATGTTGAGACTTAACTTAA 713  
 Qy 1094 GCTTGGCGAAGAGAGACATGCTGTTATGTTGTGTGTGATCAAGATGATGAGGACTATGAG 1153  
 Db 714 GCATTTGGCCAAAGAGAGACATGCTGATGATGATGATGATGATGATGATGATGATGAT 773  
 Qy 1154 GAAGCTTACGATGTCGAGTCCGAAATCTACAAAGCTGCTGACAGATATGAAAGTG 1213  
 Db 774 GAACCTTAAAGAAATAGGAATCTTAAAGTATCAAGGTTGATGACAGGACATGAGATT 833  
 Qy 1214 AATTAATTCATGCTTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1273  
 Db 834 AATTAATTCATGCTTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 893  
 Qy 1274 CGACACGCGCAAGAGCATTTATGAGGCGACAGACAGAAATTAATGAGCGCATGAT 1333  
 Db 894 CGCATATTTGAAATGATATATATGATGATGATGATGATGATGATGATGATGATGATGAT 953  
 Qy 1334 TTTGTTTGAAGCGCGCTGTGAGGTTCTTGTGCAAGTTCATAGCGCGGCTGTCCCTTAT 1393  
 Db 954 TTTGTTTGAAGCGCGCTGTGAGGTTCTTGTGCAAGTTCATAGCGCGGCTGTCCCTTAT 1453  
 Qy 1394 GGGATGGAATATCGTGTGTTATTTGCAATGATTTGACACAGGACACTCTGCTGTAT 1453  
 Db 1014 GGAATGGAATTTGTTTTCATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1073

QY	1454	CTGGAACCATATTTACAGGACCAATGAGTTTATGACAGACACTGGCTCCATTATAGATATA	1513
Db	1074	TTGAAAGCAGTGTTCCTGTAATCGTGANTTAATGACATACGCTGCTGTCTTGTTATTT	1133
QY	1514	CATPACATCGCGCACCGAGGCGGTGGCCCACTAGATGAATTCCTCGTTACACCGAGTTGCTT	1573
Db	1134	CACAAACATTTGACATCAGGGTCTGGTGTCCGTTAGATATATCTTCATATGTGGATTGGCA	1193
QY	1574	GAGCACTACCTGGAAACCTTCAAGCTGTACACCCCTGGGTGTGAGCAGGCCAATAC	1633
Db	1194	CATATACATATGACTGTTTAGCTGATGATTCCTGTGGAGGTGAGCATTTTAACATT	1253
QY	1634	TTGCGCGCGGCTGAAGATGGCGACCAAGTTGTCTGTGTGAGCCCGGATCCTGTGG	1693
Db	1254	TTTGCACCTGGTATAAAGACTGCTGACCCGTGTGTATACAGTTACCAATGGCTTAGCTTGG	1313
QY	1694	GAGCTCAAGACGATGAGGGGCGGCTGGGGGCTTACACACATCATACGACGAAACGACTGG	1753
Db	1314	GAGTTTAAATCATGTGAAGTGTGTGGGATTTGATATAGANTCATCAAGATGTCATTTGG	1373
QY	1754	AAGACCCGCGGCACTGCTACACGCAATGACAACAATGAGTGGAAACCCGAGTGGACGTC	1813
Db	1374	AAATTTCAATGATATTGTAAATGAATGATACCATATGTTGAATCCAAATTTTGACGCT	1433
QY	1814	CACCTCAAGTGGACGGCTACACCAACTTCTCCCTGGGAGCGTGGACTCCGCGCAACGG	1873
Db	1434	CACTTAAATTTGTATGTTTACCAACAATTGACCTGGAAATCTTTGAATGGAAAGGCC	1493
QY	1874	CAGTGCMAAGAGGCGCTTGCAGCGGAGCTGGGCTTGCAGTCTGGCGCGCATGTCCGCTG	1933
Db	1494	CAGTGCMAAGGCTGTTTGGCAACGAGAGTTTGTCTGCTGTTCGTGACGAGTTCATATT	1553
QY	1934	CTCGGCTTCATCGGCGCGCTGAGCGGAGCGGAGAGGGCGTGGAGATCATTCGCGGACCATG	1993
Db	1554	CTTGCCTTCATTGGGAGATTTAGCCATCAAAAAGTATATAGATCTATAGCGGAGGCCATG	1613
QY	1994	CCCTGGATCTGTGAGCCAGAGAGCTGACGTGGTCACTGTCTGGGACCCGCGCCACAGACTG	2053
Db	1614	CATGGGCTGTGTGGCAAGATCTACAGATTAATCATGTGGGACCTGGGAGGCCACAGACTTC	1673
QY	2054	GAGAGCATCTGCGGCACTTGCAGCGGAGGACCAACAAGAGTGTGCGGGTGGGTGGG	2113
Db	1674	GAGAGATATGCTTCGAAGATTTGAACGTGAGCATGCGGTTAAGTCAAGGAGATGGGTGGG	1733
QY	2114	TTTCTCCGTGCGCTTGGCGCACCGGATCAACGCGGGCGCGGACGGCTCTCATGCGCTCC	2173
Db	1734	TTTCTCAGTAAATATGGCTCATGTGATCAAGAGGTGTGATGCCCTTACTATGCTGCTCC	1793
QY	2174	CGGTTTCGAGCGGTGCGGGTGTGAACCAAGCTTTTACGCGCATGAGCTTACGCGCACCGTCCGCTC	2233
Db	1794	AGGTTTCGAACCTTGTGTGATTTGAACCAACTTCACGCTATGATGTATGGAACAATTCCTGTT	1853
QY	2234	GTCACGCGCGCTTGGCGGGGTGAGGGACACCGGTGCGCGCTTGCACCTTTGAACAACCTCC	2293
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QY	2294	GGCCTCGGAGTGAACCTTGCACCCGCGCGAGGCGCAACAAGCTGATGAGAGCGCTCGGAGAC	2353
Db	1914	GATTTCGGATGTGACCTTTGACAGGGCAGAGGACATPAGATGATGTGGCACTCGGCAT	1973
QY	2354	TGCCCTCCGACCTTACCGGAGCTTACAAAGAGAGTGGAGGGGCTCAAGAGCGGCGCATG	2413
Db	1974	TGCTTAAACATATTCGGAATTTACAGAGAACTGGTGGATTCAGAGAGGAGATG	2033
QY	2414	TGCGACAGCTTCAGCTGGAGCATGCGCGCAAGCTCTACGAGAGCTCCTCTCAAGGCC	2473
Db	2034	ATGCAGAGACTCAGTTGGAGAGTGTGTGCGGACCATATGAAAAAGTCTCTTGTGCTGCC	2093
QY	2474	AAGTACCAATGGTGA 2488	
Db	2094	AGTATCAATGGTGA 2108	

```

RESULT 14
US-08-836-567-7
; Sequence 7, Application US/08836567
; Patent No. 6130367
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; APPLICANT: Springer, Franziska
; APPLICANT: Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENE
; TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,567
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04415
; FILING DATE: 09-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 41 408.0
; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Agrevo14
; TELECOMMUNICATION INFORMATION:
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2793 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Solanum tuberosum
; STRAIN: cv Desiree
; TISSUE TYPE: leaf tissue
; IMMEDIATE SOURCE:
; LIBRARY: cDNA-library in Lambda ZAP11
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 242..2542
; US-08-836-567-7
Query Match 25.3%; Score 717.8; DB 3; Length 2793;
Best Local Similarity 67.3%; Pred. No. 1e-135;
Matches 1013; Conservative 0; Mismatches 492; Indels 0; Gaps 0;
QY 984 CCGGACCTTTGGCCAGGSGAAGACGTCATGAACTGTGCTGCTGCGCTGCGTGAATGCTCTC 10433
DB 1041 CCCCTCCATGTGGCAGAGAAACAATGATGTATGAACATTATTTGTGGCTTCACAAATGCCCTC 11000
QY 1044 CCTGTGCAAAACAGGTGCTCTTGGAGATGTTGCCCGGTCTTTGCCAAGGCTTTGGCGA 11033
DB 1101 CATGTGCTAAACAGGTGGGCTTGGAGATGTTGCTGGAGCATTAACCAAGCTTTGGGCTC 11600
QY 1104 AAGAGAGACATGCTTTATGTGTGTGGTATCCAAAGTATGGGGGACTATGAGAGACCTTAGC 11633

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Db 1161 GACGTGGCCACAGAGTTATGTTGTGGACCTCTGTATGACAACTATCTGAACTCAAG 1220  
 Qy 1164 ATGTGAGAGTCCGAAATATACTACAGAGCTGTGACAGATATGGAAGTGAATTTATTC 1223  
 Db 1221 ATTCGGGTGTAAGAAAAATTTATAAAGTTGATGGATGGAGTGAAGTGAATTTCTC 1280  
 Qy 1224 ATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1283  
 Db 1281 AAGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1340  
 Qy 1284 AAGAACATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1343  
 Db 1341 GGAACAACTTTACGAGAGGAAACGCTGTGATATTTTAAACGATGATTTATTTTGA 1400  
 Qy 1344 AGGCGCTGTGAGAGTTCCTTGGACGTTTCAATGGGCGGCTCCCTATGAGGATGAA 1403  
 Db 1401 AAGCAGCAGTATGAGTTCCTTGGACGTTTCAATGGGCGGCTCCCTATGAGATGAA 1460  
 Qy 1404 ATCTGATGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1463  
 Db 1461 ATTATGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1520  
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 Qy 1524 CGCACCAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1583  
 Db 1581 CTCATCAGGCGTGTGCTTCTTGGAGATTTTCAATGATGATGATGATGATGATGATG 1640  
 Qy 1584 TGGACACTTTCAGACTGTACAGACCCCGTGGTGTGAGACGCGCAACTTTCGCGCGG 1643  
 Db 1641 TGGACCTTTCAGACTGTACAGACCCCGTGGTGTGAGACGCGCAACTTTCGCGCGG 1700  
 Qy 1644 GCCTGAAGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1703  
 Db 1701 GTCTAAGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1760  
 Qy 1704 CGGTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1763  
 Db 1761 CTTCACAGGCGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1820  
 Qy 1764 GCATGCTCAACGCGCATGCAACAATGATGATGATGATGATGATGATGATGATGATG 1823  
 Db 1821 GTATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1880  
 Qy 1824 CGGACGCTTACCAACTTCTCTCTGGGAGCGTGTGATGATGATGATGATGATGATG 1883  
 Db 1881 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1940  
 Qy 1884 AGGCGCTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1943  
 Db 1941 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2000  
 Qy 1944 TCGGCGGCGTGTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 2003  
 Db 2001 TTGGGAGGCTTGAACCAACAAAGGCGTGTGATGATGATGATGATGATGATGATG 2060  
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 Db 2061 TGGGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2120  
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 Db 2121 TAAGGCAATTTGAGTGTCAACACATATATAAATTAAGAGATGGTGTGTTCTCTGTA 2180  
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 Db 2301 TAGAGGATCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2360  
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 Db 2541 GGTGA 2545

RESULT 15  
 US-09-606-304-7  
 Sequence 7, Application US/09606304  
 Patent No. 6483010  
 GENERAL INFORMATION:  
 APPLICANT: Kosseman, Jens  
 Applicant: Springer, Franziska  
 TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: FISH & NEAVE  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10020  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/606,304  
 FILING DATE: 28-Jun-2000  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/836,567  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: DE P 44 41 408.0  
 FILING DATE: 10-NOV-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Haley Jr., James F.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: Agrevo-4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-596-9000  
 TELEFAX: 212-596-9090  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2793 base pairs  
 TYPE: nucleotide  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 ORIGINAL SOURCE:  
 ORGANISM: Solanum tuberosum  
 STRAIN: cv D. str.e



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2004, 17:53:38 ; Search time 971 Seconds

(without alignments)  
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Title: US-10-018-418-3

Perfect score: 2842

Sequence: 1 gctgcacacccctcgcctg.....aaaaaaaaaaaaaaaaa 2842

Scoring table: IDENTITY NUC

Gapop 10\*0, Gapext 1.0

Searched: 2308684 seqs, 1750822206 residues

Total number of hits satisfying chosen parameters: 4617368

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications NA:\*

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- 18: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2392.2	84.2	2825	9	US-09-952-677-5
2	1238.6	43.6	2412	15	US-10-260-238-1034
3	989.4	34.8	1110	15	US-10-260-238-3323
4	806.6	28.4	2418	14	US-10-044-543-25
5	784	27.6	2269	12	US-10-424-599-59744
6	737.4	25.9	2348	14	US-10-044-543-5
7	717.8	25.3	2793	14	US-10-284-668-7
8	711.4	25.0	1926	14	US-10-284-668-5
9	644.2	22.7	662	15	US-10-260-238-4322
10	451.6	15.9	632	15	US-10-260-238-4324
11	268.6	9.5	682	15	US-10-260-238-4016
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15	246.8	8.7	2263	14	US-10-272-291-2

16	205.4	7.2	934	15	US-10-260-238-4015	Sequence 4015, Ap
17	201.6	7.1	1449	15	US-10-369-493-28444	Sequence 2844, A
18	201.6	7.1	1449	15	US-10-369-493-31203	Sequence 3120, A
19	195.8	6.9	2223	14	US-10-228-063-9	Sequence 9, Appl
20	195.8	6.9	2239	9	US-09-952-677-1	Sequence 1, Appl
21	192	6.8	1383	15	US-10-369-493-44603	Sequence 4460, A
22	188.6	6.6	2360	14	US-10-284-668-9	Sequence 9, Appl
23	176.6	6.2	1377	15	US-10-369-493-42867	Sequence 4286, A
24	171.4	6.0	1758	14	US-10-284-668-3	Sequence 3, Appl
25	162.4	5.7	617	12	US-10-424-599-59740	Sequence 59740, A
26	162.2	5.7	1440	15	US-10-369-493-35062	Sequence 3506, A
27	162.2	5.7	1440	15	US-10-369-493-38466	Sequence 3846, A
28	162.2	5.7	1440	15	US-10-369-493-38650	Sequence 3865, A
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30	160.4	5.6	1428	15	US-10-369-493-44118	Sequence 4411, A
31	149.8	5.3	1446	15	US-10-369-493-35988	Sequence 3598, A
32	143.4	5.0	2202	14	US-10-044-543-1	Sequence 1, Appl
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34	137.8	4.8	1461	15	US-10-369-493-26666	Sequence 2666, A
35	136.6	4.8	1419	15	US-10-369-493-33675	Sequence 3367, A
36	133.6	4.6	1158	12	US-10-424-599-73305	Sequence 7330, A
37	129.2	4.5	1386	15	US-10-369-493-39252	Sequence 3925, A
38	129.2	4.5	1386	15	US-10-369-493-39632	Sequence 3963, A
39	129.2	4.5	1386	15	US-10-369-493-40000	Sequence 4000, A
40	127.8	4.5	2176	14	US-10-044-543-13	Sequence 13, Appl
41	127.2	4.5	1443	15	US-10-369-493-34260	Sequence 3426, A
42	125.4	4.4	1398	15	US-10-369-493-33582	Sequence 3358, A
43	121.6	4.3	564	14	US-10-044-543-17	Sequence 17, Appl
44	121.6	4.3	564	12	US-10-424-599-138092	Sequence 1380, A
45	121.2	4.3	2399	14	US-10-158-075-1	Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-09-952-677-5  
Sequence 5, Application US/09952677  
Patent No. US20020138876A1  
GENERAL INFORMATION:

APPLICANT: Block, Martina

Lutz, Horst

Luticke, Stephanie

Walter, Lemart

Frohberg, Claus

Kossmann, Jens

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES  
FROM WHEAT WHICH ARE INVOLVED IN STARCH  
SYNTHESIS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/952,677

FILING DATE: 14-Sep-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/196,390

FILING DATE: 19-NO. US20020138876A1-1998

APPLICATION NUMBER: DE 196 21 588.9

FILING DATE: 29-MAY-1996

APPLICATION NUMBER: DE 196 36 917.7

FILING DATE: 11-SEP-1996

APPLICATION NUMBER: PCT/EP97/02793

FILING DATE: 28-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley, Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: AGR-9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2825 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Trifolium aestivum L.  
STRAIN: cv. Florida  
TISSUE TYPE: ca. 21 d Caryopses  
IMMEDIATE SOURCE:  
LIBRARY: cDNA library in pBluescript sk (-)  
CLONE: pTAS81  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 162..2559  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-952-677-5

Query Match 84.2%; Score 2392.2; DB 9; Length 2825;  
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Matches 2613; Conservative 0; Mismatches 108; Indels 66; Gaps 9;

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 Db 1736 TCCACTCAAGTCGAGCGGCTACACCACTTCTCCCTGCGGAGCGTCGTCGTCGTCGTCGTCG 1795  
 QY 1872 GCGAGTCAGAGAGCGGCTGTCGAGCGGAGCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1931  
 Db 1796 GCGAGTCAGAGAGCGGCTGTCGAGCGGAGCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1855  
 QY 1932 TCGTCGCTTCAATCGGCGGCTGTCGAGCGGAGAGAGCGTCGTCGTCGTCGTCGTCGTCGTC 1991  
 Db 1856 TCGTCGCTTCAATCGGCGGCTGTCGAGCGGAGAGAGCGTCGTCGTCGTCGTCGTCGTCGTC 1915  
 QY 1992 TCGCTGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2051  
 Db 1916 TCGCTGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1975  
 QY 2052 TGGAGAGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2111  
 Db 1976 TGGAGAGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2035  
 QY 2112 GGTTCCTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2171  
 Db 2036 GGTTCCTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2095  
 QY 2172 CCGGCTCGAGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2231  
 Db 2096 CCGGCTCGAGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2155  
 QY 2232 TCGTCGACCGCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2291  
 Db 2156 TCGTCGACCGCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2215  
 QY 2292 CCGGCTCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2351  
 Db 2216 CCGGCTCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2275  
 QY 2352 ACTGCTTCGACCTACCGGATCAAGAGAGCTGAGAGGCTTCAGAGCGCGGCA 2411  
 Db 2276 ACTGCTTCGAGACGTACCGGATCAAGAGAGCTGAGAGGCTTCAGAGCGCGGCA 2335  
 QY 2412 TGTGCGAGACCTTACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2471  
 Db 2336 TGTGCGAGACCTTACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2395  
 QY 2472 CCAAGTACAGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2531  
 Db 2396 CCAAGTACAGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2412

## RESULT 3

US-10-260-238-4323

; Sequence 4323, Application US/10260238

; Publication No. US20040016025A1

; GENERAL INFORMATION:

; APPLICANT: Budworth, Paul R.

; APPLICANT: Moughamer, Todd G.

; APPLICANT: Briggs, Steven F.

; APPLICANT: Cooper, Bret

; APPLICANT: Glazebrook, Jane

; APPLICANT: Goff, Stephen A.

; APPLICANT: Katagiri, Fumiyuki

; APPLICANT: Kreps, Joel



QY	1212	TGAATATTTCATGCTTTAATACAGATGAGAGTTGATTTTGTTTCATTTGACAGCCCTCT	1271
Db	878	TAACATTATTCATGCTTTAATACAGAGGTGGATTTTGTTTATGAGATGATCCAGACT	937
QY	1272	TCGACACCGCCACGAGAACATTATGCGGCGACGACACAGAAATTATGAAACGATGA	1331
Db	938	TCCGTACACCGGGGAATCGTATTTTATGAGGGAACACAGTGGATCTTAAACGATGA	997
QY	1332	TTTGTGTTCTCAGAGCGCGCTGTGAGAGTTCCTTGAGCAGTTCATGCGGGGAGTCCCTT	1391
Db	998	TTTTGTCTTCAGAGCAGCTGATGAGGTTCTTGGCATGTTCCATGAGTGGGCTTCGT	1057
QY	1392	ATGGGGAATGGAATCTGTGTTTATTGCAATGATTGGCACAGGCACTCTGCTGTCT	1451
Db	1058	ATGAGATGGTATTTTGGCTTTCATCAAGAAATGATGGCATACTGCTCTCTGCGCTGT	1117
QY	1452	ATCGAAGACATTTACAGAGACCATGTTTATGACAGTACACTCGGTCCATTAATGATGA	1511
Db	1118	ATCGAAGACATTTATGCTGACAAATGCGTGAATATATGCTCGGTCTGTTCTGTATGA	1177
QY	1512	TACATAACATCGCGGACACAGGGCGCTGGCCGATGATGATGATTCCTCGTTACCGAGTTC	1571
Db	1178	TACACACATGAGCCACCGAGGTGATGATCTGTGATGATGATCTCAATTTGTGGGCTGTC	1237
QY	1572	CTGAGCACTACTGGAACACTTCAACATGTAACGACCCCGTGGGTGTGAGCACAGCCAACT	1631
Db	1238	CGGATCACTACTTGGACCTTTTCAATTTATGACCCCGTGGAGGGAACATCTCATTA	1297
QY	1632	ACTTCGCGCGCGGCTCGAAGATGGCGGACACAGGTTGTCTGTGTAGTCCCGGATACGT	1691
Db	1298	TTTTGTGTGTGCGCTGGAAGACTGCTGACCAAGTGTACTGTATGACATGTTATGAT	1357
QY	1692	GGGAGCTCAAGAGCGTGTGAGGGCGGCTGCGGCTTTCACGACATCATACGCGAGAAAGACT	1751
Db	1358	GGGAGCTGAHAACATCAGAAAGGTGTGGGCGTACATGAATTAATTAATGAAGATTA	1411
QY	1752	GGAAGACCCCGGCACTCTCAACCGCATCTGACAAATGATGTGAACCCCGAGGTGTGAC	1811
Db	1418	GGAAGTTTCAAGGATTTGTAATGTGATTTGATGCAAGAGGTGAGGCCCGAATTTGATG	1477
QY	1812	TCCACCTCAAGTGTGAGCGGCTACACAACTTCTCCCTGCGGAGCGCTGCACTCCGCGAAGC	1871
Db	1478	TGCACCTTAATCCGATGTATCACAATTAATCTCTAGATTACTTTAGATGGGTAAGC	1537
QY	1872	GCGAGTGAAGAGGCGCTGTGAGCGCGGAGCTGGGCGTGTGAGGTTCCGCGCCAGATGACCGC	1931
Db	1538	CAGATGTATGAGGCTGCTTTTGACGACGAGGTGGTCTGCTGTTCTGTGATTAATGTACCA	1597
QY	1932	TGCTCGGCTTCATCGGCGCGCTGTGACCGGACGAAGGCGTGTGAGATCATTCGCGAGACCA	1991
Db	1598	TCATTTGATTCATTGTGAGAGGTTAGACCAACAGAAAGCGTGCATCTCATTTGCGAGGACCA	1657
QY	1992	TGCGCTGGAATCGTGACCCGAGCGTGTGACGCTGTGATGCTGTGGGACCGCGCGCACAGAC	2051
Db	1658	TGCGTTGATTTGTCACTGTATGTATTTCAAATGATCTATTAATGAGACGAGGAGTAAAGC	1717
QY	2052	TGAGAGCATGCTGTGCGGACCTTTCAGCGGAGACCAACGACAAAGTGTGCGGAGTGGGTGTG	2111
Db	1718	TTTGAATTTTACTGAGAGAACTTTGAGCGGTCAACACAGGGAACAAATTTAGACATGGGTGTG	1777
QY	2112	GGTTTCGCGGCGCTGTGTGACACCGGATTCACGGGCGGGCGCGAGCGGCTCTCATGCGCT	2171
Db	1778	CATTTTCAATTAAGATGTGCGCATTAATTAACAGAGGTGCGGACATCTCTATGATGCTTT	1837
QY	2172	CCCGGTTTCGAGCCGTGCGGTTTGAACACAGCTTTTACGCAATGCGCTTACCGCACCGGTCCCG	2231
Db	1838	CGAGGTTTGAAGCATTCGGATTTGAACACAGCTTTTACGCAATGATGTATGACACCATTTCCAG	1897
QY	2232	TGCGTACGCGCGCTCGGCGGAGTGAAGGACACCGTGTGCGGCTTTCGACCCCTTCAACACT	2291
Db	1898	TGTGTGATGTGTGTGGGGCGCTTATGAGATCAAGTGAATCTCAATTTGATCTTTTCACAGGT	1957
QY	2292	CGCGCTCTGGGTGAGCTTTGACCGCGCGGAGGCGCACAACTGATTCAGAGCGCTTGGCG	2351

Db	1958	CTGTCCTTGGTTGGACCTTGACACAGGGCACAAGGAGAAGACTGCATGCCATTGTAAATA	2017
Qy	2352	ACTGCTCCCGCACTTACC GGGA CTACAGAGAGCTGGAGGGCCTCCAGAGCGCGCA	2411
Db	2018	ACTGCTTGAATATCATCTGGAATTACAGAGACAGTTGGAGGGCTCTTCAACAAGAGGGA	2077
Qy	2412	TGTGCGAGGACCTTAGCTGGAGAGCATGCCCAAGCTCTACAGAGAGCTCTCCCTCAAG	2471
Db	2078	TGATGCAAGACTTAGCTGGGATATATCTCTCAGCAATACAGAGATGTCTCTTGTTCAG	2137
Qy	2472	CCAAGTACCACTGGTGA	2488
Db	2138	CCAAGTACCAATGGTGA	2154
 RESULT 5 US-10-424-599-59744 ; Sequence 59744, Application US/10424599 ; Publication No. US20040031072A1 ; GENERAL INFORMATION: ; APPLICANT: La Rosa Thomas J ; APPLICANT: Kovalic David K ; APPLICANT: Zhou Yuhua ; APPLICANT: Cao Yongwei ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With ; FILE REFERENCE: 38-21(5323)B ; CURRENT APPLICATION NUMBER: US/10/424,599 ; CURRENT FILING DATE: 2003-04-28 ; NUMBER OF SEQ ID NOS: 285684 ; SEQ ID NO 59744 ; LENGTH: 2969 ; TYPE: DNA ; ORGANISM: Glycine max ; FEATURE: ; OTHER INFORMATION: Clone ID: PAT_MRT3847_24960C.1 US-10-424-599-59744			
 Query Match                      27.6%; Score 784; DB 12; Length 2969; Best Local Similarity        69.1%; Pred. No. 1,1e-190; Matches 1072; Conservative    0; Mismatches 480; Indels    0; Gaps    0;			
Qy	944	GATGATCGGCGCTCTTGAAACATCACAGAACATGATCCGGACCTTGGCAGGGAG	1003
Db	972	GCTAATGAGGCGCAATGTGAGAGGTAAAGGTAAAAACCCCCACCGTGGCTGGGGCC	1031
Qy	1004	AAGCTCATGAACGTGTGCTGTGGCTGCTGAATGTTCTCCCTGTCCAAACAGGTGT	1063
Db	1032	AATGTTCATGAATGTCATTTGGTTGGCAGAGAAATGTCTCCCTCGTCAAAACAGGTGT	1091
Qy	1064	CTTGAGAGTGTGCGCGGTGCTTGGCCCAAGGCTTTGGCGAAGAGAGACATCGGTATG	1123
Db	1092	CTTGGAATGTGCTGCGATCATTACTTAAGGCTTTGGCTTAGGGGTGGACACAGATTATG	1151
Qy	1124	GTGTGTGTACCCAGGTATGGGACTATGAGAAAGCTCAGATGTGGAGTCCGAAAATAC	1183
Db	1152	GTTGTAGACTCCGTTAGTACATTAATGCTGACGSCACAMATATAGAGATGGAACGA	1211
Qy	1184	TACAAGCGTGTGACAGAGATATGGAAGTGAATTAATTCATGCTTATATCATGAGT	1243
Db	1212	THCAAGATGATGTGTGAGACATGGAAGTAAATATTTCCACTTTATATGATGTGTT	1271
Qy	1244	GATTTGTGTTCAATGAAGCTCTCTCTTCGACACCGCAGAGAGACATTATGGGGC	1303
Db	1272	GACTTCGTTTTATATGACAGTCCMAACCTTTCGCAATTAACAGGTAAACATATATGGGGGA	1331
Qy	1304	AGCAGACAGAAATTAAGAGCGCATATTTGTTCTGCAAGGCGGTGTGAGATTCT	1363
Db	1332	AACGAGAGGATATTTCAAAACGATGTGTGTTTTCAGAGGAGCTGTGAGATTCT	1391
Qy	1364	TGGCAGTTTCATGCGCGGTGTCTCTTATGGGAGTGAATCTGTGTTTATTCGAAT	1423

Db	1392	TGGCAGTGTCTCTTGAGTGGAGTTTGCTATGAGAAATGGAATTTGGCCTTCATCGCAAAAT	1451
Qy	1424	GATTGGGACACGGCAGCTCCGCTGCTCATCTGAAGAAGCAATTAACAGGGACCATGGTTGG	1483
Db	1452	GATTGGCATCTGCTTTGGCTGCCAGGTATCTGAAGACATATTAATGCTGACCATGGTTTAA	1511
Qy	1484	ATGCAAGTACACTCGGCTGCATTTATGGTGATACATTAACATCGCGCACCAAGGGCCGTGGCCCA	1543
Db	1512	ATGAAGTACACAAGATCTGTTCTTGATTCATTAACATACACACACCGAGGAGCGGGCCCCC	1571
Qy	1544	GTTAGTAAATTTCCCGTTTCCACCGAGTTGGCTGAGAGTACCTGGAACAATTGACATCTGAC	1603
Db	1572	ATTATATATTTCCGCTACACAGATTTTACCTGACACATACATAGACCTTTTCAAAATTATAT	1631
Qy	1604	GACCCCGTGGGTGGTGGAGCACGCCAACTACTTCGCGCGCGCTGAAGATGGCGGACAG	1663
Db	1632	GACCCGGTGGAGGTGGAGCACTTCAAAATCTTTTGGCTGGTTTAAAGGACGCTGACCGG	1691
Qy	1664	GTTGTGCGGTGGAGACCCCGGGGTACTCTGGGGAGCTCAAGACGCGTGAAGGGCGGCTGGGGG	1723
Db	1692	ATTGTCACTGTGATCTGATGATATGATCATGGAGATTTAAACTTTGAAAGGTGCTGGGGCT	1751
Qy	1724	CTTCACGACATCATACGGCAGACAGCATGGAAGACCGCGGACATGTCACACGCAATGCAC	1783
Db	1752	TTGCATGGGATCATTAATGAGAAATGACTCGGAAATTTGAGAGGAATTTGAAATGGAAATTGAC	1811
Qy	1784	AAACAATGAGTGGAAACCCCGAGGTGGAGGTCCACCTCAAGTGGAGCGGCTACACCACTTC	1843
Db	1812	ACCAAAAGTTGAAACCCCAAGATTGATGTTTACTTGAATATAGATGATACATTAATCTAC	1871
Qy	1844	TCCCTGGGAGCGTGGACTCCGGCACGCGCAGTGCACAGAGGCCCTTGACAGCGGACTG	1903
Db	1872	ACCCTTGAGACCTTCGCAAGTGGCAGAGGCTGACATGCAAAAGCCGCTTGCAAAAGAACTC	1931
Qy	1904	GAGCTGCAGGTCCGCGCGCAGGTGCGCTGCTCGGCTTATCGCGCGGCTGAGCGGACAG	1963
Db	1932	GATTTCCTGTCCGTGGAGATGTTCCGTTACTTGATTCATTTGGAAGGCTGGATCAACAG	1991
Qy	1964	AAGGCGGTGAGATCATCGCGGACGCCATGCCCTGGATCTGAGTGCAGAGCATGTGACGTG	2023
Db	1992	AAAGGCATTTGATCTCATATGACCGAAGCAATTCCTTGATATGTTGGCGCAGGAATGTCACTA	2051
Qy	2024	GTCATGCTGGGACACGGGCGGCACACACTGGAGAGACATGCTGGGCACTTCGAGCGGGAG	2083
Db	2052	GTCAATTTGGGAATCTGGAAGCCGGACTTAAAGATATGCTTAAAGCAATTTGAATGCCAA	2111
Qy	2084	CACCAACGACAAGTCTCGCGGATGGGTGGGGTTCTCCGTGCGCTGGCGCACCGGATCACG	2143
Db	2112	CACCGTGCACAAAGTACAGAGATGGGTTGGCTTTTGGTGCACAGATGCTCACCGGATAACA	2171
Qy	2144	GGGGCGCGCGACGCGCTCCTCATGCGCTCCCGGTTGCGAGCGGTGCGGTTGAACCACTT	2203
Db	2172	GAGGTGCGACATATTTGCTGATGCAATCAATTTGAGGCAATGGAATTTGATCACTC	2231
Qy	2204	TACGCCATGGCCTTACGGCACCGCTCCCGCTGTGCAAGCCGCTGGCGGGGTGAGGGACAC	2266
Db	2232	TATGGCATGAAATTAACGAAACAATTCAGATTGACATGCTGCTGGTGAATTGAGGGATVCA	2291
Qy	2264	GAGCGGCGCTTGCACCCCTTCAACACACTCGGCTCGGTTGAGACCTTCGACCCGCGCAG	2322
Db	2292	GTGMAAGCTTTTAATTCATTGGAAGTGGGCTTGGGTGGAATTTGACAGTGCAGAA	2355
Qy	2324	GGGCACAGCTGATCGAGGCGCTCGGGCACCTGCTCCGACCTTACCGGGAATTAAGAGAG	2388
Db	2352	ACTTAACAAATTTAATAATCATTAAGGAATCTGTTGACCTTACAGGCAATTAAGGACAG	2411
Qy	2384	AGCTGAGAGGGCTTCAGAGAGCGCGGACATGTGCGACGACATTGAGCTGGAGCATGCGCC	2443
Db	2412	AGTGTGGGAAGGCTCCACAGCGGAGGAGTGAACGACAGATCTTAAGTTGGGACATCTGCT	2471
Qy	2444	AAGCTTACAGAGACGTCTCTCTCAAGGCCAATTAACATGGGTGAACGGTAG	2495
Db	2472	CAGCAATATGAGGAGTCTTGTGTGCTGTCAATGATACAAATGGAATTTCTTG	2523

	RESULT 6	
	US-10-044-543-5	
	/ Sequence 5, Application US/10044543	
	/ Publication No. US20030135893A1	
	/ GENERAL INFORMATION:	
	/ APPLICANT: Singletary, George	
	/ APPLICANT: Zhou, Lan	
	/ TITLE OF INVENTION: No. US20030135893A1el Search Synchase Polynucleotides	
	/ TITLE OF INVENTION: and their use in the Production of New Starches	
	/ FILE REFERENCE: 114AD	
	/ CURRENT APPLICATION NUMBER: US/10/044,543	
	/ PRIOR FILING DATE: 2002-01-11	
	/ PRIOR APPLICATION NUMBER: 09/388,743	
	/ PRIOR FILING DATE: 1999-09-02	
	/ NUMBER OF SEQ ID NOS: 28	
	/ SOFTWARE: FastSeq for Windows Version 3.0	
	/ SEQ ID NO 5	
	/ LENGTH: 2348	
	/ TYPE: DNA	
	/ ORGANISM: Curcuma zedoaria	
	/ FEATURE:	
	/ NAME/KEY: CDS	
	/ LOCATION: (36) ... (2105)	
	US-10-044-543-5	
	Query Match	25.9%; Score 737.4; DB 14; Length 2348;
	Best Local Similarity	67.9%; Pred. No. 9.2e-179;
	Matches 1029; Conservative	0; Mismatches 486; Indels 0; Gaps 0;
Oy	974 AACCATGATTCGGACCTTTGGCGAGGAGAAAGTCACTGAACGTCGTGCTGCCT	1033
Dd	594 AATCGAACCTCTCCTCTTGCTGCTGCCATATGTAATATATCATATTGTAAGCTGCA	653
Oy	1034 GAATGTTCCCTCGTGCMAAACAGTGTCTTGSAGATGTTGCCGCTCTTCCCAG	1093
Dd	654 GAATGTGACCATGGTCTTAAAACAGTAGGCTTGGAATGTTGTGAAGCTTTAACT	713
Oy	1094 GCTTTGGGAGAAGAGGACATCGTGTAATGTTGTGATCCCAAGGTATGGGACTATAG	1153
Dd	714 GCATTGGCCAAAGAGAGACATGATGATCATGTAATGTTCTCCAAATATGAAAACTAT	773
Oy	1154 GAAGCTACGATGTGAGAGTCCGAAATATCTACAAGCTGCTGACAGGATATGGAAGT	1213
Dd	774 GAACCTAAGAAATAGGAATCTTAAAAGGTACAGGTTGATGACAGGACATGAGANT	833
Oy	1214 AATTAATTCANCTTATATGATGAGAGATGATTTGGTCATTGACGCTCCTCTTC	1273
Dd	834 AAATCTATCATCTTACCTACATGATTCGTATGTAATTTGCTTCAACGATAGTCTATTT	893
Oy	1274 CGACACCGCACAGAAACATTTATGAGGCGACGACACAGAAATTANGAGCGCATGAT	1333
Dd	894 CCCCATATGGAATAATATATATATGATGAAAACGAGTGGACATTTTGAAAGATGGTA	953
Oy	1334 TTGCTTGTGAAGCGCGTGTGAGAGTTCCTTGGACGTTTCCATGCGGCGGTGCCCTTAT	1393
Dd	954 TTTGTTGTGAAGCGACAGTGTAGTTCCTTGGACATGTCATATGATGAGATTCGTAT	1013
Oy	1394 GGGAGTGAATCTGAGTGTATTTGCAAATGATTTGGCAACGAGCATCTCTGCTGTAT	1453
Dd	1014 GGAGATGGGAATTTGATTTTCAATTCACCAAGTTGGCATPACCTCTTATCTTCCAGTTAT	1073
Oy	1454 CTGAAGCATTTATTAAGGAGACATGTTGATGAGTCACTCGGCTCATTTATGATGATA	1513
Dd	1074 TTGAAGCATGTTTCCGTATGATGATGATTAATGATAATAGCTCGCTGTCTGTGGTATAT	1133
Oy	1514 CATACATGCGCACACGAGGCGCTGTGGCCAGTAAATGAAATTTCCGTACACGAGTGTGCT	1573
Dd	1134 CACACATTTGCACATCAAGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1193
Oy	1574 GAGCATTAATGGAACCTTCAAGCTGTATGCAAGCCCGGTGTGTGTGTGTGTGTGTGTGTGT	1633

Mon Feb 23 11:51:12 2004

us-10-018-418-3.rnpb

**ପୃଷ୍ଠା ୫**

Db	1199	CATGATCACTATGATCTCGTTTGAAGCTGGATGATCTCTTTGAGGTGAGACTTTTAACTT	1253
Oy	1634	TTGCGCCGCGGAGCTCAAAATGGCCGAGACCAAGTTTGCTGGTGAAGCCCGGGGTACTGTGG	1693
Db	1254	TTTGCAAGCTGGTATTAAGAGCTGCTGACCGTGTGGTTCAAGTATAGCCATGCTATGCTTGG	1313
Oy	1694	GAGCTCAAGACGGTGGAGGGCGGCTGGGGCTTTCACAGATCTAAACGCGAGAACACTGG	1753
Db	1314	GAGTTAAAAAATCTGAAGTGGTGGGATTTGATGATGATCTATCAACAGATGGCCATTGG	1373
Oy	1754	AAAGACCGGGGACATGCTCAAGCGGCAATGCAACAATGAGATGAAAGCCCGAGGTGAGACATC	1813
Db	1374	AAATTCCATGCTATTGTAAATGGAAATCGATTCACATAGTTGGATCCAAAATTTAGACGT	1433
Oy	1814	CACCTAAAGTCGAGACGGCTTACCAACTTCTCTCGGGAGCGTGGACTTCGCGCAAGCGG	1873
Db	1434	CAGTTAAATTCTGATGTGTTACACCAACTTCAACCTCGAAGAACTTTAAATGGAGAAAGGC	1493
Oy	1874	CAGTGAAGAAGGCGCTCGAGCGGCAAGCTGGGCGCTGAGGTTCGCGCCGACAGTGGCGCTG	1933
Db	1494	CAATGCAAGGCTGCTTTGACAGAAATTTGGTCTGCTGTGTGTGTAACAGACGTTCCTATT	1553
Oy	1934	CTGGGCTTCACTCGGCGCGCTTGGAGCGGGAGAAAGGGCGTGGAGATCATTCGCGAGCGCATG	1993
Db	1554	CTTGGCTTCAATTGGAGATTAGACCATTAAGAAAGTTAAATCTCAATAGGAGAGCCATG	1613
Oy	1994	CCCTGGATCGTAGGACGAGACAGTGCAGCTGCATGTCTGGGACACCGAGCGCACAGACTG	2053
Db	1614	CACCTGGCTCGTGGCTCAAGATCTACAGATAATCATGTCTGGGCACTGGAGAGGCCAGCTGC	1673
Oy	2054	GAAAGATCTGTGGGGAATTTGACAGGGGAGACCAACAGAAAGTTCGCGGGTGGTGGGG	2113
Db	1674	GAGGATATGTCTGAAGATTGAACGTAGACATGCGGTAAAGTCAGGGGATGGGTGGG	1733
Oy	2114	TTCTCCGTGGCCTTGGCGACGACCGAATCAACGCGGGCGCCAGCGGCTCTCATGACCCTTC	2173
Db	1734	TTCTCAATGAATAATGCTCATCGAATCAACAGAGTGTCAATGCTCATGAGCCCTCC	1793
Oy	2174	CGGTTGGAAGCGCGGGGTTGAACAAGCTTTAAACGCAATGCGCTACACGACCCGCGCCGC	2233
Db	1794	AGGTTTGAACCTTGTGGATTGAACCACTTCAACGCTATGATGTAAGCAACATTTCTGTT	1853
Oy	2234	GTCGACGCGCGTCCGCGGGGTGAAGGACACCGTGCACGCGCTTCAACCCCTTCAACACTTC	2293
Db	1854	GTCGATGCAATAGTGTGCTTTCGAAATATCTGTGCAACAGTTTGTATCCGTTCAATGAGACA	1913
Oy	2294	GGCTCTGGGTGAGACGTTTCGACCGCGCCGAGGGCGCAACAGCTGATCGAGGCGCTCGGGCAC	2353
Db	1914	CGTTTGGATGAGACTTTTGAACAGGGCAGAGGACATAGATGATAGTGGCACTCGGCCAT	1973
Oy	2354	TGCTCTCCGCACTTAACCGGACATACAGAGAGCTGAGAGGGGCTTCCAGAGACCGGCGCATG	2413
Db	1974	TGCTTAACCAATATGGAAATTACAGAGGAGCTGGGGGTGATTGCAAGAGCGAGGAGATG	2033
Oy	2414	TGCGAGACTTCAAGCTGGGAGCATCGCCCAAGCTCTACAGAGACGTCCTCTCAAGGCC	2473
Db	2034	ATGAGAGCACTCAAGTTTGGAGAGTGTGCGGACGACTATGAAAAAAGTCTTGTGTGTCGC	2093
Oy	2474	AAAGTAAACAGTGTGTA 2488	
Db	2094	AAAGTAAACAGTGTGTA 2108	

```

RESULT 7
US-10-284-668-7
; Sequence 7, Application US/10284668
; Publication No. US20030106100A1
GENERAL INFORMATION:
APPLICANT: kossmann, Jens
           Springer, Franziska
           Abel, Gernot
TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
                     INVOLVED IN STARCH SYNTHESIS VECTORS
                     BACTERIA TRANSGENICALLY

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PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/284,668
FILING DATE: 29-Oct.-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,567
FILING DATE: 24-JUL-1997
APPLICATION NUMBER: PCT/Ep95/04415
FILING DATE: 09-NOV-1995
APPLICATION NUMBER: DE P 44 408.0
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Agrevo-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2793 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Solanum tuberosum
SPRAIN: cv Desiree
TISSUE TYPE: leaf tissue
IMMEDIATE SOURCE:
LIBRARY: cDNA-library in Lambda ZAPIT
FEATURE:
NAME/KEY: CDS
LOCATION: 242..2542
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
? ? ? ? ?
US-10-284-668-7
Query Match      25.3%   Score 717.8; DB 14; Length 2793;
Base Local Similarity 67.3%; Fred. No. 1e-173;
Matches 1013; Conservative 0; Mismatches 492; Indels 0; Gaps 0
QY 984 CCAGACCTTTGGCAGGAGGAGAAGCAATGAACGTGTCGTGCGTGCCTGTAATGTTCTC 1043
DB 1041 CCCCTCATGGCAGAAACAATGTATTGAACATATTGTTGGTGCTTCAGATGGGCTC 1100
QY 1044 CCGGTGGCAAACAAGTGTCTTGAGATGTTGCCGTGCTTGCCCAAGGCTTTGGGGA 1109
DB 1101 CATGGCTTAAACAAGTGGCTTGGAGATGTTGCTGGAGCATTAACCAAGCTTTGGCTC 1166
QY 1104 AGAGAGACATCGTGTATGTTGTGTGCCAAGTATGSGGACTATGAGAAAGCTTAG 1165
DB 1161 GAGGTGGCACAGAGATTATGTTGTGGACCTCGTTATGCAACTATCCTGAAGCTCAG 1220
QY 1164 ATGTGGAATCCGAAAATACTACAAGAGCTGCTGGACAGATATGGAAGTGAATTAATTC 1223
DB 1221 ATTCTGGTGTAAAGAAAAATTATAAAGTTGATGTGTAGATGTGGAAGTGAATTAATTC 1280
QY 1224 ATGCTTATATGATGAGATGATTTTGTGTTTCAATGACGTCTCTCTTCGACACCGGC 1283

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Db	1281	AAGCTTTATGATGCGTGGAATTTGGTTTTCATATGACAGTCAATATGTTTAGACATG	1340
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Qy	1884	AGGCCCTGACGCGGAGCTGGGCGCTGACGATCGCGCGGACGTCGCGCTCGCGCTCA	1943
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us-10-018-418-3.rnpb

Page 10

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? LOCATION: 2..1675
? OTHER_INFORMATION: /function= "Polymerization of
? starch"
? /product= "Starch synthase"
? SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-284-668-5

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Query Match	25.0%;	Score 711.4;	DB 14;	Length 1926;
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Matches 1009;	Conservative	0;	Mismatches 496;	Indels 0;
			Gaps	0;

Qy	98	CCGACCTTTGGGAGGGAGGAACGCTATGAACCGTGGTCCGTGGAGCTCGAATGTTCC	104
Db	174	CCCTTCATTTGGCGAGGAACAAATGTATGAACATATTTGGTGGCTTCAGAAATGGCTC	233
Qy	1044	CTGTGTCAAAAACAGGTGTCTTGSAGATGTGGCCGGTCTTTGCCCAAGCTTGGCGA	1103
Db	234	CATGTGCTAAAAACAGGTGGCTTGGAGATGTGGTCGAGATTAACCAAAAGCTTGGCTC	293
Qy	1104	AGAGAGACAAATGTGTATGTGTGGATGGATACCAAGTATGGGGACTATAGGAAGCTACG	1166
Db	294	GACGTGGCCACAAATGTATGTGTGGACCTCTGTATGCAACTATCTCGAAGCTCGAG	353
Qy	1164	ATGTGGAGTCCGAAAATACTACAAAGCTGTGACAGGATATGAAATGGAATTAATTC	1223
Db	354	ATTCTGTGTAAAGAAAATTTATTAAGTGAATGTGACGATATGGAAGTACCTTAATTC	413
Qy	1224	ATGCTATATTCGATGGAGTGAATTTGTGTCATTTGACGCTCCCTTCGACACCGCC	1288
Db	414	AACTTTTATTAATGTGTGGATTTTGTTCATTTGACATGATCAATGTTTAAACACATTG	473
Qy	1284	AGGAGACATTTATGGGGGACAGACAGAAATTAAGAACGATGATTTGTCTGCA	1343
Db	474	GGAAACAACATTTACGAGAGGAAACCTGTGATATTTTAAACCAACAGTTTATTTTGA	533
Qy	1344	AGGCGCTGTCAAGTCTCTTGGACGCTTCATCGCGCGATGTCCCTTATGGGGAATGGA	1408
Db	534	AAAGACGATTTAGAGTTCCTTGGCATTTCCATGTGGTGGGGTCTGTATGGAGATGAA	593
Qy	1404	ATCTGGTGTATTTGCAAATGATTTGGCACACGCACTCTGCTGTCTATCTGAAAGAT	1463
Db	594	ATTATATGTTCAATCTCTATATGATGGCACTAGCTTTTATGGCAGTAACTCTGAAAGCTT	653
Qy	1464	ATTACAGGAGCAATGTTTGAATGACATCACTCGCTCATTTATGGATATCAATAATCG	1522
Db	654	ATTATGTGTACATGGAATTAAGAACTATACAAATCTGTCTGGATTCATACATCG	713
Qy	1524	CGCACAGGACCGTGGCCCAAGTAAGATTTCCGTTACCCAGTTCCTGACACTACC	1583
Db	714	CTCATCAGAGGTGTGTGCTCTTTGGAGATTTTTCATATGTAGATCTTCCACCACTATA	773
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Qy	1944	TGGGGCGCGCTGGACGGGGCAGAGGGGCGTGGAGATCATGCGGGACCGCATGCCCTGGATGCG	2003
Dh	1134	TTCGGAAGGCTTGACCCCAAAAGGGGTGTTATCTGATTTCTGAGGCGCACTGCTTGGATGCA	1139
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Dh	1194	TGGGTTCAGATGTAAATGTGGTCACTGTTGGGAGCGGGAGGCGGTGACTCTTGAACAGATGCG	1253
Qy	2064	TGGCGCACTTCAGCGGGAGACCCACGACAAAGGTGCGCGGTGGTGGGGTTCTCCGTGCG	2123
Dh	1254	TAAAGCAATTTAGTGTCAACACAAATGATAAATTAGAGGATGGGTGGTTTCTCTGTGCA	1313
Qy	2124	GCGTGGCGCACCGGATCAACGGCGGGGGCGGACGCGCTCCCTCATGCGCTCCGGTTGAGAGC	2189
Dh	1314	AGACTTCTCATGTGTAATCTGCTGTGCAACATCTGCTCATGCTTTTAAGATTGGAG	1373
Qy	2184	CGTGGCGGTTGAACCAAGCTTTACGCGATGCGCTTACGGCACCGTCCCGTGTGCAACGCCG	2243
Dh	1374	CTTGGCACTGATCAACCAAGCTTTATGCAATGAAATATGGACTATTCCTGTTGTTCAATGAG	1433
Qy	2244	TGGGCGGGGTGAGGACACCGCTGCGCGCTTGACCCCTTCAACCACTCCGGCCTCGGAGT	2303
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Qy	2424	TGAGCTGGGAGATGCGCGCCCAAGCTCTTACAGAGAGCGTCCCTGTCAGAGGCAAGTCCAGT	2483
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RESULT 9			
US-10-260-238-4322			
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Publication No. US20040016025A1			
GENERAL INFORMATION:			
APPLICANT: Budworth, Paul R.			
APPLICANT: Moughamer, Todd G.			
APPLICANT: Briles, Steven P.			
APPLICANT: Cooper, Bret			
APPLICANT: Glazebrook, Jane			
APPLICANT: Goff, Stephen A.			
APPLICANT: Katagiri, Fumiyaki			
APPLICANT: Kreps, Joel			
APPLICANT: Provost, Nicholas			
APPLICANT: Rieke, Darrell			
APPLICANT: Zhu, Tong			
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION			
FILE REFERENCE: 60111-NP			
CURRENT APPLICATION NUMBER: US/10/260,238			
CURRENT FILING DATE: 2002-09-26			
PRIOR APPLICATION NUMBER: US 60/325,448			
PRIOR FILING DATE: 2001-09-26			
PRIOR APPLICATION NUMBER: US 60/325,277			
PRIOR FILING DATE: 2001-09-26			
PRIOR APPLICATION NUMBER: US 60/370,620			
PRIOR FILING DATE: 2002-04-04			
NUMBER OF SEQ ID NOS: 6077			
SEQ ID NO 4322			
LENGTH: 662			
TYPE: DNA			



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1  GENERAL INFORMATION:
2  APPLICANT: Budworth, Paul R.
3  APPLICANT: Moughamer, Todd G.
4  APPLICANT: Briggs, Steven P.
5  APPLICANT: Cooper, Bret
6  APPLICANT: Glazebrook, Jane
7  APPLICANT: Golf, Stephen A.
8  APPLICANT: Katagiri, Fumiyuki
9  APPLICANT: Kreps, Joel
10 APPLICANT: Provart, Nicholas
11 APPLICANT: Ricke, Darrell
12 APPLICANT: Zhu, Hong
13 TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
14 FILE REFERENCE: 6011-NP
15 CURRENT APPLICATION NUMBER: US/10/360,238
16 PRIOR FILING DATE: 2002-09-26
17 PRIOR APPLICATION NUMBER: US 60/325,448
18 PRIOR FILING DATE: 2001-09-26
19 PRIOR APPLICATION NUMBER: US 60/325,277
20 PRIOR FILING DATE: 2001-09-26
21 PRIOR APPLICATION NUMBER: US 60/370,620
22 PRIOR FILING DATE: 2002-04-04
23 NUMBER OF SEQ ID NOS: 6077
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25 LENGTH: 682
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28 US-10-260-238-4016

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OY      2310 TCAGCCGCGCGGAGGCGGCACAAGACTGATCGAGGCGCTCGGAGCACTGCTCCGACCTACTAC 2368
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OY      2430 GGGAGCATGCGCGCAAGCTCTAAGAGAGAGCTCTCTCAAGGCGCAAGTACCAAGTGTGA 2488
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; Sequence 7, Application US/10228063
; Publication No. US20030135885A1
; GENERAL INFORMATION:
; APPLICANT: Lanahan, Mike
; TITLE OF INVENTION: Self-processing Plants and Plant Parts
; FILE REFERENCE: 109846.317
; CURRENT APPLICATION NUMBER: US/10/228,063
; CURRENT FILING DATE: 2002-12-12
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; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 1818
; TYPE: DNA

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Qy 2443 CAGCTTACGAGGAGCGTCTCTCTCA 2468  
Db 1713 CAAGAAGTGGGAGAGAGTCTCTCA 1738

## RESULT 13

US-09-961-077-25  
Sequence 25, Application US/09961077  
Publication No. US20030014775A1  
GENERAL INFORMATION:

APPLICANT: Zwick, Michael G.  
Edington, Brent B.  
McSwigen, James A.  
Merlo, Patricia Ann Owens  
Guo, Lining  
Skokut, Thomas A.  
Young, Scott A.  
Folkerts, Otto  
Merlo, Donald J.  
TITLE OF INVENTION: COMPOSITION AND METHODS FOR  
MODULATION OF GENE EXPRESSION  
IN PLANTS

NUMBER OF SEQUENCES: 1263  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700

CITY: Los Angeles  
STATE: California

COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/961,077  
FILING DATE: 21-Sep-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/679,645  
FILING DATE: July 12, 1996  
APPLICATION NUMBER: 60/001,135  
FILING DATE: July 13, 1995  
APPLICATION NUMBER: 08/300,726  
FILING DATE: September 2, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 219/247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 955-0440  
TELEFAX: (213) 955-0440  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2267 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
US-09-961-077-25  
Query Match 8.8%; Score 250; DB 10; Length 2267;  
Best Local Similarity 52.3%; Pred. No. 9.9e-54;  
Matches 798; Conservative 0; Mismatches 650; Indels 78; Gaps 8;  
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Db 413 CGGCATGAGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 472  
Qy 1066 TGAAGATGTTGCGGCTTTCGCAAGCTTTCGCAAGAGAGAGACATCGTTATGAT 1125  
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Qy 1246 TTTTGTGTTGATGAGAGCTCTCTCTCC-----GACACCGCGCAGAGAGA 1290  
Db 653 CCGCGTGTGTTGATGAG 712  
Qy 1291 CATTTA-----TGGGCGCAGCAGACAGAGAAATTATGAGAGCGCATGTTTGT 1338  
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Qy 1339 CTGCAAGGCGGCTGCGAGGTTCTTGGACGTTCCATGCGGCGGAGTGTCTTATGAGGAG 1398  
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Db 893 GTGCTACCTCAAG 952  
Qy 1507 GGTATACATGAG 1566  
Db 953 CTGATCAACAAGATCTTACAG 1012  
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Db 1013 CTTCCGAGAGATTCAGTCGCTTCTGATTTCAATCCAGCGCTACGAGAAACCGGTGA 1072  
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Qy 2029 GCTGAGACCGCGCGCGCACTGAGAGAGATGCTGCGGCACTTGAAGCGGAGACCA 2088  
Db 1478 GCTGAGACCGCGCGCAAGAGAGTTCAGAGGCTCATGAGAGCGCGAGAGAGATTTCC 1537  
Qy 2089 GACCAAGTGCAGCGGCTGAGTGAAGTTCCTGCGCGCTGAGCGGACCGGATCAGCGGAG 2148  
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## RESULT 14

US-10-272-291-1  
; Sequence 1, Application US/10272291  
; Publication No. US20030150023A1  
; GENERAL INFORMATION:  
; APPLICANT: Exseed Genetics  
; TITLE OF INVENTION: Starch  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/272,291

; CURRENT FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: 60/329,525  
; PRIOR FILING DATE: 2001-10-01  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2263  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Wild type sequence EX385  
US-10-272-291-1

Query Match 8.7%; Score 248.4; DB 14; Length 2263;  
Best Local Similarity 52.2%; Freq.No. 2.6e-53;

Matches 797; Conservative 0; Mismatches 651; Indels 78; Gaps 8;

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Qy 1507 GGTGATACATATGAG 1566  
Db 958 CTGATCTCAAG 1017  
Qy 1567 GTTGTGAG 1614  
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Qy 1615 TGGTGAAGCAGCGCACTTTCGCGCGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1674  
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Job time : 981 secs
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Mon Feb 23 11:51:12 2004

us-10-018-418-3.rst

Page 1

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 22, 2004, 14:32:44; Search time 6434 Seconds  
(without alignments)  
13190.599 Million cell updates/sec

Title: US-10-018-418-3

Perfect score: 2842  
Sequence: 1 gctgcaccacccctccgctg.....aaaaaaaaaaaaaaaaaaaaa 2842

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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2: em\_escba.\*  
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26: em\_escba.\*  
27: em\_escba.\*  
28: gb\_esc1.\*  
29: gb\_esc2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1210	42.6	3248	11	AY111778 Zea mays
2	991.2	34.9	2498	11	AY109714 Zea mays
3	633.8	22.3	1003	29	CG037054 PUKER30TD
4	623.4	21.3	780	14	CD892632 G118.1211

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C	6	583.8	20.5	785	14	CD443882	CD443882
C	7	579.8	20.4	655	13	BQ246237	TAR1501AE
C	8	573.6	20.2	638	13	BQ608768	BRY 4680
C	9	566.5	19.9	871	29	CG260010	OG0E221TH
C	10	563.8	19.8	871	29	BM137830	MB137830
C	11	560	19.7	870	29	CG260024	OG0E221TV
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C	14	539.2	19.0	566	14	CA600087	waw1c.pko
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C	17	510.6	18.0	550	14	CD895576	G174.100D
C	18	510.2	18.0	637	14	CD929519	GR45.108G
C	19	509.8	17.9	537	14	CD930574	GR45.111L
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C	23	494.2	17.4	600	14	CD895922	G174.101F
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## ALIGNMENTS

RESULT 1	AY111778	3248 bp	MRNA	linear	HTC 17-OCT-2002
LOCUS	AY111778				
DEFINITION	Zea mays CL171.1 mRNA sequence.				
ACCESSION	AY111778				
VERSION	AY111778.1	GI:21216366			
KEYWORDS	HTC				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 3248) Hartney,C.F., Dolan,M., Mao,G.H., Vogel,T.M., Whitsett,M.S., Arthur,L.W., Hanafey,M., Morante,M., and Tinney,S.V.				
TITLE	Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes				
JOURNAL	Unpublished (2002)				
REFERENCE	2 (bases 1 to 3248) Coe,E.H.				
AUTHORS	Direct Submission				
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA				
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZMD and may be found by BLAST searching at MSU, maizegap.crg; ZMD, www.zmd.iasate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the				

maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schmale, Iowa State, then clones may be requested from ZMDB:  
www.zmdb.iastate.edu.

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Location/Qualifiers  
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/clone\_lib="Maize Mapping Project/Dupont Cornsensus Library"

/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

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Query Match 42.6%; Score 1210; DB 11; Length 3248;  
Best Local Similarity 83.0%; Pred. No. 5.3e-150;  
Matches 1354; Conservative 0; Mismatches 277; Indels 0; Gaps 0;

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QY 983 TCCGAGACCTTTGGAGGAGAGAGATCATGAGGCTGCTGATGAGGCTGAGGCTGAG 1042  
DB 1356 TCTGGGCTTTGGCGCGGAGAGATGTTAAGAGCTGATGCTGCTGCTGAGGCTGAG 1415  
QY 1043 CCTGGTGCAGAAAGAGTGTCTTGAAGATTTGCCGCTTTGCCAGGCTTTGGCG 1102  
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QY 1643 GGCCTGAAGATGAGGAGCAGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 1702  
DB 2016 GGTGTGAAGATGAGGAGCAGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 2075  
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QY 2243 GTGCGGAGGAG 2302  
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RESULT 2  
AY109714 2498 bp mRNA linear HTC 17-OCT-2002  
LOCUS AY109714  
DEFINITION Zea mays Cl17L\_2 mRNA sequence.  
ACCESSION AY109714  
VERSION AY109714.1 GI:2213541  
KEYWORDS HTC.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;



Mon Feb 23 11:51:12 2004

us-10-018-418-3.rst

Page 4

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RESULT 3	LOCUS	DEFINITION
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REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (Passes 1 to 1003)	Whiteclaw,C.A., Quackenbush,J., Van Aken,S., Utechtack,T., Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennettzen,J	Maize Genomics Consortium	Unpublished (2003)	Other_GSSs: PUXE3J0TB

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Qy	2101	CGGGTGGGTGGGGATTCTTCGCTGGGCGCTGGGGGACACCGGATTCACGGGGGGCCCGACCGCGCT	2160
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Qy	2221	CACCGTCCCCGCTCGTGACAGCCGCTCGGCGGGGTGAAGGACACCGTGGCCGCTTGACCC	2280
Db	541	CACCGTCCCTGTGGTGGACAGCCGCTGGGCGGGCTCAAGGACACCGTGGCGCCGCTTGACCC	600
Qy	2281	CTTCAACAACCTCCGGGCGCTCGGGGTGAGATTGACCGCGCGAGAGGCGCAACAAGCTGATCGA	2340
Db	601	GTTCACGCGAGCGCGGGGCTCGGGTGGACTTTTGAACCGCGCGAGGCCACACAGCTGATGGA	660
Qy	2341	GGCGGCTCGGGACCTGGGCTCGGCACTTACCGGGACTTACAAGAGAGCTGAGGGGCTTCCA	2400
Db	661	GGGCGCTCAAGGACCTGGGCTCGGCACTTACCGGAGCTTACGAGAGAGCTGGAAAGTCTCCA	720
Qy	2401	GGAGGCGGCGCATGTGCGAGGACTTCAAGCTGGGAGCATGCGCGCAAGCTTTACGAGGAGCT	2460
Db	721	GGGCGCGGCGCATGTGCGAGGACTTCAAGCTGGGAGCATGCGCGCTTGAAGCTTTACGAGGAGCT	780
Qy	2461	CCCTCCCTCAAGGCGAAGTACCAAGTGGTGAACGCT	2493
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RESULT 4					
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LOCUS	GI:112109R010927	GI:18	Triticum aestivum	cDNA clone	GI:18121109.
DEFINITION	mRNA sequence.				
ACCESSION	CD892632				
VERSION	CD892632				
KEYWORDS	CD892632.1	GI:32663166			
SOURCE	EST.				
ORGANISM	Triticum aestivum (bread wheat)				
	Triticum aestivum	112109	Embryonata	Tychochrysa	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 780)	Genoplatante.	Genoplatante, a major partnership french program in plant genomics	Unpublished (2003)	Contact: Genoplatante
	Genoplatante	93, rue Henri Rochefort 91025 EVRY CEDEX France		
		Tel: 33 1 69 47 54 00		
		Fax: 33 1 69 47 54 10		
		This sequence has been generated in the framework of the french		
		plant genomics programme 'Genoplatante' ( <a href="http://www.genoplatante.com">http://www.genoplatante.com</a>		
		and <a href="http://genoplatante-info.infobiogen.fr">http://genoplatante-info.infobiogen.fr</a> ).		
FEATURES		Location/Qualifiers		
SOURCE		1..780		

301 CGGGAGCGCATCCCTGATCGCGGGCAGACCTGCACCTGGTATCTCTGGGACACCG 360  
2041 CCGCACGACCTTGAGAGCATCTCGGCACTTGAGCGGAGCACCACGACAAAGTGGC 21000

Query March	21.9%	Score 623.4	DB 14	Length 780
Best Local Similarity	91.6%	Pred. No. 1.3e-72		
Matches 733	Conservative 0	Mismatches 41	Indels 26	Gaps 6
1959 GGCAGAAAGCGCTGGATTCATCCGGCGAGCCATCCCTGATTCGTGAGACAGACATCC 2018				



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Db      776  GGGCAAGGCGGTGGAGATCATTCGGACCCGATG-CCTGGAATCGTGAACCGA--ACGTC 720
Qy      2019 AGCTGTGCTAATGCTGGGACACCGGCGCCGACGACTGGAGAGCATGTGCGGCACTTCGAGC 2078
Db      719  AGCTGTGCTAATGCTGGGACACCGGCGCCGACGACTGGAGGCAATTCGCGGCACTTCGAGC 660
Qy      2079 GGGAGCAACCAACGCAAGAGTGGCGGGTGGGTGGGTTCTCCGCGGCCCTGGGCGGCAACCGGA 2138
Db      659  GGGAGCAACCAACGCAAGAGTGGCGGGTGGGTGGGTTCTCCGCGGCCCTGGGCGGCAACCGGA 600
Qy      2139 TCAAGGCGGCGCGCGGCTCTCTATGCGCTCCCGGTTTCAGACCGCTGCGGATTGAAC 2198
Db      599  TCAAGGCGGCGCGCGGCTCTCTATGCGCTCCCGGTTTCAGACCGCTGCGGATTGAAC 540
Qy      2199 AGCTTTACGCCATGCGCTTACGCGACCGTCCCGCTCTGTCACGCGCTCGCGGGGTGAAGG 2258
Db      539  AGCTCTACGCGCATGCGCTTACGCGACCGTCCCGCTCTGTCACGCGCTCGCGGGGTGAAGG 480
Qy      2259 ACAACCGGCGCGCGGTTGAGACCCCTTCAACCACTCCGCGCTCGGGTGAAGCGTTGAC 2318
Db      479  ACAACCGGCGCGCGGTTGAGACCCCTTCAACCACTCCGCGCTCGGGTGAAGCGTTGAC 420
Qy      2319 CCGAGGCGCAACAGCTGATCGAGCGCGCTCGGGGACCTGCTCCGACCTACCGGAGCTACA 2378
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Qy      2499 CTAGCCGCTCCAGCGCCGCGCATGCGTGAATGATAGAGGAGTGAACCTGGCGCC 2558
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Qy      2559 GCAGAGAGCTGACCTCTCTCTGATGAGAGCGCGCATCCGCGAGGTGACAGTACATGA 2618
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Qy      2679 GAGGTGTGTGTGTGAGACGCTGATTCGATCTGATCTGATCTGATCTGATCTGATCTGAT 2738
Db      82  GAGGTGTGTGTGTGAGACGCTGATTCGATCTGATCTGATCTGATCTGATCTGATCTGAT 23
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RESULT 5  
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 LOCUS OG30P68TV ZM 0.7.1.5 KB Zea mays genomic clone ZMMBMA0776L16,  
 DEFINITION genomic survey sequence.  
 ACCESSION CG362560  
 VERSION CG362560.1 GI:34279827  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 798)  
 Whitehead, C.A., Quackenbush, J., Van Aken, S., Uteerback, T.,  
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
 Citek, R.W., Nuneberg, A., Robbins, D. and Lakey, N.

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TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Other GSSs: OG30P68TV
Contact: Cathy Whitehead
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitehead@tigr.org
Seq primer: TP
Class: sheared ends.
FEATURES
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  1587 AACACTTCAAGCTGTAGACACCCGCTGGTGTGAGACGCGCACTACTTCGCCCGCGCC 1646
  Db      796  AACATTGAGCTGTAGATCCCGCTGGTGTGAGACGCGCAATCTTTCGCGGCTC 737
  Qy      1647 TGAATATGCGGACCAAGGTTCGTGTGAGAGCCCGGATACCTGTGGAGCTCAAGACG 1706
  Db      736  TGAATATGCGGACCGGTGTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAG 677
  Qy      1707 TGAAGGCGGCTGGGAGCTTCAACGATCATTCGCGAGACGATCTGGAAGCCGCGCA 1766
  Db      676  TGAAGGCGGCTGGGAGCTTCAACGATCATTCGCTTCAAGACTGTGAAGTCAATGCA 617
  Qy      1767 TGTCAAGCGCATTCACAAATGAGTGAACCCCGAGTGAACGCTCCAGCTCAAGTCCG 1826
  Db      616  TGTGAACGCGATTCACCAACGAGTGAACCCCGAGTGAACGCTCCAGCTCAAGTCCG 557
  Qy      1827 ACGGCTACCACTTCTCTCTGAGAGCGCTGAGCTCCGCGCAAGCGGAGTGAAGAG 1886
  Db      556  ACGGCTACCACTTCTCTCTGAGAGCGCTGAGCTCCGCGCAAGCGGAGTGAAGAG 497
  Qy      1887 CCTTGAAGCGGAGCTGGGCTCTGAGAGTCCGCGCGAGTGGCGGTCTGAGCTCATCG 1946
  Db      496  CCTTGAAGCGGAGCTGGGCTCTGAGAGTCCGCGCGAGTGGCGGTCTGAGCTCATCG 437
  Qy      1947 GCCGCTGAGCGGAGCGGAGCGGCTGAGAGTCCGCGCGAGTGGCGGTCTGAGCTCATCG 2006
  Db      436  GCCGCTGAGTGAAGAGAGGAGTGAATCATATCGGGAGCGCATGCGGTGATCGCGG 377
  Qy      2007 GCCAGAGCTGAGCTGTGATCTGTGAGACCGCGCGCGCGAGCTTGAAGAGAGTCCG 2066
  Db      376  GCCAGAGCTGAGCTGTGATCTGTGAGACCGCGCGCGCGAGCTTGAAGAGAGTCCG 317
  Qy      2067 GGCATTTCGAGCGGAGCGACCAAGAGTGTGGGTGGGTGTCTCCGTGCGCG 2126
  Db      316  AGCACTTGAAGCGGAGCGATCCCAAGAGTGTGGGTGGGTGTCTCCGTGCGCG 257
  Qy      2127 TGGCGACCGGATCACGCGCGCGCGCGAGCGCTCTCATGCGCTTCCCGGTTCGAGCGCT 2186
  Db      256  TGGCGATCGCATCACGCGCGCGCGCGAGCGTGTGATGCGCTTCCCGGTTCGAGCGCT 197
  Qy      2187 GCGGTTGAACAGCTTTCAGTGCATAGGCTTACGCGACCGCTCCCGTGTGAGCGCGCTG 2246
  Db      196  GCGGTTGAACAGCTTTCAGTGCATAGGCTTACGCGACCGCTCCCGTGTGAGCGCGCTG 137
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Db	136	GGCGGCTCAGGGAGCAACCTGCGCGCTTCGACCCGTTACAGCGACGCGCGGCTCGGCTGGA	77		
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Db	76	CTTTTACCGGCGCGAGGCGCAACAAAGCTGATTCGAGGGGCTCGGAGCACTGCTCCGCAACGT	17		
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RESULT 6	CD443882	795 bp	mRNA	linear	EST 03-JUN-2003
LOCUS	EC01N0432C10.b	EndospERM_4	Zea mays	cDNA, mRNA sequence.	
DEFINITION	CD443882				
ACCESSION	CD443882				
VERSION	1				
KEYWORDS	EST.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 795)				
TITLE	Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and Messing,J				
COMMENT	Sequencing of the maize endospERM ESTs				
JOURNAL	Unpublished (2002)				
CONTACT	Contact: Lai, Jinheng				
COMMENT	Dr. Joachim Messing's lab				
COMMENT	Waksman Institute, Rutgers University				
COMMENT	150 Frelinghuysen Rd., Piscataway, NJ 08854, USA				
COMMENT	Tel: 732-445-5801				
COMMENT	Fax: 732-445-5735				
COMMENT	Email: jlai@waksman.rutgers.edu				
COMMENT	Seq primer: T3.				
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Best Local Similarity	84.3%;	Pred. No. 2.1e-67;			
Matches 657;	Conservative	0;	Mismatches 122;	Indels 0;	Gaps 0;
1419	CAATGATTGGCAGCAGCGGCACTCTGCTCTCTATCTGAAAGCATTTACAGGACCATG	1478			
Db	4	CGAGGGATTGGCAGCAGCTGCACTCGCTCTGTTATCTGAAGGCAATTTACAGAGCAATG	63		
Qy	1479	GTTTGAAGCAGTACACTCGATCGATTCATTAAAGTAAACATTCGCGCAGCGGCGCG	1538		
Db	64	GTTTAAAGCAGTACACTCGATCGATTCATTAAAGTAAACATTCGCGCAGCGGCGCG	123		
Qy	1539	GCCCAAGTAAATTCCTGTTCCAGAGTTGCTTGAGCACTACCTGGAACATTTCAAC	1598		
Db	124	GTTCTGTAGTAAATTCCTGTTCCAGAGTTGCTTGAGCACTACCTGGAACATTTCAAC	183		
Qy	1599	TGTACGACCCCGTGGGTGGTGAAGCAGGCAACTACTTTCGCGCGCGGCTGAAGATGGCG	1658		
Db	184	TGTACGATCCCGTGGGTGGTGAAGCAGGCAACTACTTTCGCGCGCGGCTGAAGATGGCA	243		
Qy	1659	ACCAAGTGTGCGGTGGTGAAGCCCGGGTACCTGTGGAGCTCAAGACGTTGAGGGCGGCT	1718		
Db	244	ACCGGCTGTGACTGTTCAGCTCGGCTACCTGTGGAGCTGAAACAGTGAAGGCGCT	303		
Qy	1719	GGGGGCTTACGACATCATTCAGGCAAGAACGACTGGAAGACCCGCGGCTGTCACAGCA	1778		

Db	304	GGGGCCCTCCAGACATCATCCGTTCTTAACGACTGGAAAGATCATATGACATCGTGAACGGCA	363
Qy	1779	TCGACAACTGAGAGTGAACCCCGAGGTGAGAGTCCACCTCAAGTCGAGCGGTACACCA	1898
Db	364	TCGACCAAGAGAGTGAAGCCCAAGGTGAGCTGACCTCGGGGTGGACGGCTTACACA	423
Qy	1839	ACTTCTCCCTGGGGACGGCTGACCTCCGGCAAGCGGACAGTGCAGGAGCGCTTGCAGCGCG	1898
Db	424	ACTACTCCCTCCAGACACATTCGACGCGTGGAAAGCGGACGTGCAGAGCGGGCCCTCGACGCGG	483
Qy	1899	AGTTGGGGCTGGAGGTCCGCGCGGACGAGTGGCGGTCTGCTCGGCTTACATCGGCGGCTCGAGCG	1958
Db	484	AGCTGGGGCTGGAAATGGCGGCGACACATGTCGCTGCTTCGGCTTACATCGGCGGTCTGGAATG	543
Qy	1959	GGCAGAAAGGCGTGGAGATCATTCGCGGAGCGCATGCTCTGGAATCTGTGAAGCCAGAACGTGC	2018
Db	544	GACAGAAAGGCGTGGACATCATTCGGGGAGCCGATGCTGTGGATTCGGGGGGCGAGACGTGC	603
Qy	2019	AGCTGGTCAATGCTGGGCGACCGGCGCGACAGACCTGAGAGAGCATGCTGGGGGCACTTCGAGCG	2078
Db	604	AGCTGGTGAATGCTGGGGCACCGGGGCGCGCCAACTCGAAGAGAAATGCTGCACGACATTGGAGCG	663
Qy	2079	GGGAGACCAACAGCAAGGTGCGCGGAGTGGGTGGGGTTCTCCGTGCGCTTGCGCGACCGGA	2138
Db	664	GGGAGCATCCCAACAGAGTGGCGCGGGTGGGTTTCGGGTGCTAATGGCGCATCCCA	723
Qy	2139	TCAACGGCGGGCGGACGCGCTCTCATAGCCCTCCCGGTTGACGCGGATCGGCGGTTGAAC	2197
Db	724	TCAACGGCGGGCGGACCATGCTGTGTGAATGCTCTCCGCTTACAGGCTTCGCGGCTGACCT	782

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RESULT 7
BQ246237
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BQ246237          655 bp      mRNA      linear      EST 03-MAY-2002
TAE15014E03R TAE15 Triticum aestivum CDNA clone TAE15014E03R, mRNA
sequence.
BQ246237
BQ246237.1  GI:2042113
EST.
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 655)
Cloutier,S.
Wheat functional genomics - glenlea developing seeds cDNA libraries
Unpublished (2002)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dufour Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@agr.gc.ca
was cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >1.4 kb
Plate: 014 row: E column: 03
Seq primer: M13 Reverse.

Location/Qualifiers
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/lab_host="E. coli DH109"
/clone_1ib="TAE15"
/note="Vector: pCMV-SPORT6.0 (Invitrogen Technologies);
Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds

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VERSION	C3260010.1	GI:34169102
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SOURCE	Zea mays	
ORGANISM	Zea mays	
REFERENCE	<p> Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  clade; Panicoideae; Andropogoneae; Zea.  1 (bases 1 to 871)  Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utreback,T.,  Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,  Citek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.  Consortium for Maize Genomics  Unpublished (2002)  Other GSSs: OGOEZ21TV  Contact: Cathy Whitelaw </p>	
TITLE		
JOURNAL		
COMMENT		

FEATURES	Location/Qualifiers
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ORIGIN

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Best Local Similarity 84.3%;
Matches 638; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

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QY 1795 GAACCCCGAGGTGAGAGTCCACCTCAAGTGGAGCGCTACACCAACTTCTCCCTGGGAGC 185

Db 811 GAACCCCGGTGTGAGAGTGCACCTCCACTCCGAGCATACACCAACTACAGTTGGAGAC 752

**Qy** 185 GCTGGACCTCGGCAAGCGGCAGTGTGAAGAGGCCCTGTGCGCCGAGCCTGGAGCTTCAGAT 1914  
|||||  
|||  
**Db** 751 GTTGACACCGGCAAGCGGCAGTGTGAAGAGGCCCTGTGCGCCGAGCCTTCAGAT 692

[illegible]

Db 631 CATCATGCGGACGCGATCCATCTGATCCGCGGGGACGACGTGCACTCTGTATGTGGG 572

QY 2035 CACCGGCGGCAACGACTTGAGAGCATGCTGCGGCACTTTCGACGCGGGAGACCAAGACAA 209

Db 571 CACCGGCGGGGCCGACTTGAGAGCAATGCTGCGCGGATTGAGTCGGAACACAGCCACA 512

Qy 2095 GGTCGCGCGGATGGGATTCCTCCGATGCGCTGCGCGCACCGGATACCGGCGGGCGCCGA 215

Db 511 GGTGGCGCGCTGGGTGGGGTTCTCGGTGGCCCTGGGGCAACCGCATCAGGCGGGCGCGGA 452

Qy 2155 CGGCGTCTCATGCCCTCCGGATTGAGCGCGTGGGGTTGAACAGCTTTACGCCCATGGC 221

D8 431 CACCTCAGCAAGCCGCGGGG...CGAGTCGCCGC

D9 2215 CTACGGACAAGTCCCCGTCTGTGACAGCGCCGCGGGGTGAGGGACAACGCTGCACCCTT..227

Dy 301 CTTTCCCATCTATGCTTGCTGACACGCGGCGGGGGGCTCCGGAACAAGGTGCGCCCGT 332

QY	2275	CGAGCCCTTCAACACATCTCCGGCTCCGGATGAGACGTTGACACGGGCGGAGGCGACAAGCT	2334
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QY	2335	GATCGAGAGCGCTCGGACATCGCTCCGACACTACCGGAGTACAGAGAGACTGGAGGG	2394
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RESULT 10	568 bp	mRNA	linear	EST 28-NOV-2001
BM137830				
LOCUS				
DEFINITION				
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	library Triticum aestivum	cDNA	clone WHE0471_A06_A11	mRNA
	sequence.			

ACCESSION	BM137830	
VERSION	BM137830.1	GI:17146597
KEYWORDS	EST	
SOURCE	Triticum aestivum (bread wheat)	
ORGANISM	Triticum aestivum [Taxid:30606, Strain:cv. Stramonova; Embryonova; Tracheophyta;	

REFERENCE  
AUTHORS

Andersen, O.D., Chao, S., Han, P.S., Heinen, S., Hsia, C.C., Kang, Y.  
1 (bases 1 to 568)

Eukaryotae; Viridiplantae; Scenedesmus; Emericella;  
Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooidae; Triticeae; Triticum.

Muehlbauer G.T., Miller R.

**TITLE** The structure and function of the expressed portion of the wheat genomes - *Fusarium graminearum* infected spike cDNA library

**JOURNAL** Unpublished (2001)

COMMENT  
Contact: Olin Anderson  
US Department of Agriculture, Agriculture Research Service, Pacific  
West Area, Western Regional Research Center  
800 Buchanan Street, Albany, CA 94710, USA  
Tel: 5105595773  
Fax: 5105595718

Email: canderer@pw.usda.gov  
Fax: 3106339806

Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20. No effort was taken to identify ESTs of fungal origin from this library, thus this EST could be of wheat or fungal origin.

Seq primer: Striatogene SK primer.  
Accession: F57411.1

FEATURES  
source

LOCATION/Qualifiers  
1. .568

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/clone_id="Wheat Fusarium graminearum infected spike cDNA library"
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QY 2310 TCGACCGCGCCGAGCGGCAC 2329  
 DB 849 TCGACCGCGCGAGCGGCAGAC 868

RESULT 12  
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 mRNA sequence.  
 B0606784  
 B0606784.1 GI:21556113  
 VERSION EST  
 KEYWORDS Triticum aestivum (bread wheat)  
 SOURCE Triticum aestivum  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticaceae; Triticum.  
 1 (bases 1 to 562)  
 Clarke, B.; Lambrecht, M. and Rhee, S.Y.  
 Arabidopsis genomic information for interpreting wheat EST  
 sequences  
 REFERENCE  
 JOURNAL Funct. Integr. Genomics 3 (1-2), 33-38 (2003)  
 MEDLINE 22478026  
 PUBMED 12590341  
 COMMENT Contact: Lambrecht M  
 The Arabidopsis Information Resource  
 Carnegie Institution of Washington, Dept. of Plant Biology  
 260 Panama Street, Stanford, CA 94305, USA  
 Tel: 1 650 325 1521 x 251  
 Fax: 1 650 325 3748  
 Email: rhe@acoma.stanford.edu.  
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ORIGIN

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 DB 1 GATCGTGAAGCAGAGAGTGTGATGCTGGGAGCAGCGCCGACGACGACGCTGGAGAG 60

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 DB 61 CATGCTGGGCACTTGAAGCGGAGAGCAGACAGAGTGGCGGCTGGGCTTCTC 120

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 DB 121 CGTGGCCCTGAGCAGCGGATCAAGCGGCGCGAGCGGCTCTCATGCTCCCGGTT 180

QY 2179 CGAGCCGCTGGGCTTAACAGGCTTAAAGCCATGCTGAGGACCGCTCCCGCTGAGCA 2238  
 DB 181 CGAGCCGCTGGGCTTAACAGGCTTAAAGCCATGCTGAGGACCGCTCCCGCTGAGCA 240

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 DB 241 CGCGCTGGGCTGGGAGGAGACCGTGGCGCGCTTTCAGACCCCTTCAACAGCACTCGGAGT 300

QY 2299 CGGCTGAGAGCTTGAAGCGGCGAGAGCGGAGCAAGGCTGAGAGGCGCTCGGAGCACTGCT 2358  
 DB 301 CGGCTGAGAGCTTGAAGCGGCGAGAGCGGAGCAAGGCTGAGAGGCGCTCGGAGCACTGCT 360

QY 2359 CCGACCTACCGGAGACTACAGAGAGAGTGGAGGCGCTCCAGAGCGGCGGATGTCGA 2418  
 DB 361 NCGACCTACCGGAGACTACAGAGAGAGTGGAGGCGCTCCAGAGCGGCGGATGTCGA 420

QY 2419 GGACTTCAAGCTGGAGAGATGCGGCAAGCTCTACAGAGAGCTGCTCTTCAAGGCAAGTA 2478  
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QY 2479 CCAAGTGAAGAGCTACGCTGACCGCTCCAGCGCGGATGCTGATGATGAGAGG 2538  
 DB 481 CCAAGTGAAGAGCTACGCTGACCGCTCCAGCGCGGATGCTGATGATGAGAGG 540

QY 2539 TGAAGCTGCGGATGTCGCGCGCG 2560  
 DB 541 TGAAGCTGCGGATGTCGCGCGCG 562

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 POL1\_65\_B06\_A002 5', mRNA sequence.  
 CF480392  
 CF480392.1 GI:34509261  
 VERSION EST  
 KEYWORDS Sorghum bicolor (sorghum)  
 SOURCE Sorghum bicolor  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 721)  
 Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R., Jiang, C.,  
 Sun, F., Sullivan, R., Eastman, A., Cannon, R., Kern, B., Morgan, D.,  
 Lucas, A., Al-Sheikh, A., Jones, V., Adibi, N., Owen, A., Gao, J. and  
 Pratt, L.H.  
 EST database from Sorghum: pollen  
 Unpublished (2003)  
 JOURNAL Contact: Cordonnier-Pratt MM  
 Laboratory for Genomics and Bioinformatics  
 The University of Georgia, Department of Plant Biology  
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 583 0210  
 Email: mmprratt@uga.edu  
 Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in  
 the Human Genome Center, University of Tokyo Institute of Medical  
 Science; plant material and RNA prepared at Texas A & M University;  
 sequencing done in the Laboratory for Genomics and Bioinformatics,  
 University of Georgia. Sequence ends have been trimmed to exclude  
 vector and regions below phred quality 16. Three-prime sequences  
 are presented as their reverse complement and have been trimmed to  
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 Site 2: XhoI; The library was prepared from polyA+ RNA  
 from pollen at the late vacuolated-vacuolated stage of  
 development. Pollen was harvested from greenhouse-grown  
 panicles of sorghum line BTx623. Panicles were removed  
 from the flag leaf prior to emergence, when no detectable  
 amylase is present in pollen of male-fertile lines. This  
 stage represents pollen collected from anthers about 8-14  
 days prior to anthesis. Double-stranded cDNA was cloned  
 unidirectionally into different DraIII sites of the  
 pMR18S-FL3 vector (5-prime DraIII site is CACTGTGCG,





Mon Feb 23 11:51:12 2004

us-10-018-418-3.rst

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CD899082

LOCUS	CD893082	532 bp	mRNA	linear	EST 14-JUL-2003
DEFINITION	G174.111A1F010825	G174	Trifolium aestivum	CDNA clone	G174111A11,
RNA_SEQUENCE					

ACCESSION CD899082

**KEYWORDS** EST.

ORGANISM

REFERENCE 1 (bases 1 to 532)

TITLE Genoplante, a major partnership french program in plant genomics

COMMENT

93, rue Henri Rochefort 91025 EVRY CEDEX France

Fax: 33 1 69 47 54 10

plant genomics programme 'Genoplante' (<http://www.genoplante.com>)

and `ncpp://genoprance-into:inodrogen.117:`  
Location/Qualifiers

**SOL**

**source**

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ORIGIN

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Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 12 CCCGTCGTCAACGCCGTGAGGACACCGTGCCGCCGTTGACCCCTCAAC 71

228 CACTCCGGCTCGGGTGACGTTGACCCGCCGAGGCCACAACTGATCGAGCGCTC 2347

Db 72 CACTCCGCCCTCGGGTGAAGTTCCGACCCGCCGAGCGCACAACTGATCGAGGCGCTC 131

2348 GGGCACTGCTCCGCACTACCGGACTACAAGAGAGCTGGAGGGGCTCCAGGAGCGC 2407

Db 132 GGGCACTGCCCTCCGCACCTACCGGACTACAGGAGAGCTGGAGGGGCTCCAGGAGCGC 191

2408 GGATGTCGAGGACTTCAGCTGGGAGCATGCCGCAAGCTCTACGAGGACGTCCTC 2467

Db 192 GGCATGTCGACGACTTCAGCTGGAGCATGCCCAAGCTCTACGAGGACGTCCTCCTC 251

2468 AAGCCAGTACCAAGTGGTGAACGCTAGCTGCTAGCCGCTCCAGCCCCGCATGCGTCAT 2527

Db 252 AAGCCAAGTACCAGTGGTGAACGCTAGCTGAGCCGCTCCAGCCCCGCATGGTGCAT 311

2528 GCATGAGAGGTGGA CTGCGCATTGCGCCCGAGGA CGTGCCATCCTTCTCGATGGGA 2587

Db 312 GCATGAGAGGTGGA CTGCGCCCGAGGA CGTGCCATCCTTCTCGATGGGA 371

2588 GCGCCGCATCCGGAGGTGCAGTGCATGAGAGGTGTGTGCTTGAGACGCTGATTCC 2647

Db 372 GCGCCGCATCCGCGAGGTGCAGTGACATGAGAGGTGTGTGTGTTGAGACGCTGATTCC 431

2648 GATCTGATCTGGTCCGTAGCAGAGTAAAGCCGACGTAGGGAAGCGCTCCTTGTTCAGG 270

Db 432 GATCTGATCTGGTCCGTAGCAGAGTAGAGCGGACGTAGGGAAGCGCTCCTTGTTGCAGG, 491

2708 TATATGGGAATGTTGTCACTTGGTATTGTAGTTTG 2743

Db 492 TATATGGGATGTTCTCAACTTGGTATTGTAGTTGG 527

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